

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using bw model

Run on: March 31, 2006, 09:50:25 ; Search time 46 Seconds
(without alignments)
744.081 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTGLAIFLAVLLTVKGL.....YSEKIPSVLGIKIVNPIGK 414

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued_Patents_AA.*
2: /cgn2_6/ptodata/1/1aa/5.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/H.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCtus.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/BACKfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2130	100.0	414	2	US-09-755-665-14 Sequence 14, App1
2	2130	100.0	414	2	US-09-755-665-55 Sequence 55, App1
3	2130	100.0	414	2	US-09-755-665-56 Sequence 56, App1
4	2130	100.0	415	2	US-09-461-325-134 Sequence 134, App
5	2130	100.0	415	2	US-10-012-542-134 Sequence 134, App
6	2130	100.0	415	2	US-10-115-123-134 Sequence 134, App
7	1798	84.4	361	2	US-09-755-665-57 Sequence 57, App1
8	842	39.5	377	2	US-10-037-417-66 Sequence 66, App1
9	798	37.5	394	2	US-08-481-534-6 Sequence 6, App1
10	792	37.2	394	2	US-08-481-534-11 Sequence 11, App1
11	791	37.1	394	2	US-08-002-202-6 Sequence 9, App1
12	790	37.1	394	1	US-08-553-488A-1 Sequence 6, App1
13	785	36.9	394	1	US-09-755-665-58 Sequence 58, App1
14	785	36.9	394	2	US-09-023-339-1 Sequence 1, App1
15	785	36.9	394	1	US-08-121-714-3 Sequence 3, App1
16	785	36.9	418	1	US-08-477-108A-3 Sequence 3, App1
17	785	36.9	418	1	US-08-477-112-3 Sequence 3, App1
18	785	36.9	418	2	US-10-030-330-3 Sequence 3, App1
19	785	36.9	418	4	PCT-US93-08322-3 Sequence 3, App1
20	785	36.8	394	1	US-08-002-202-11 Sequence 11, App1
21	784	36.8	394	1	US-08-002-202-9 Sequence 9, App1
22	783	36.6	414	2	US-10-000-489-92 Sequence 92, App1
23	780	36.6	414	2	US-09-518-098B-19 Sequence 19, App1
24	776	36.4	360	2	US-10-037-417-67 Sequence 17, App1
25	772.5	36.2	414	1	US-08-002-202-17 Sequence 17, App1
26	772	36.2	414	2	US-08-481-534-17 Sequence 17, App1
27	772	36.2	414	1	US-08-481-534-17 Sequence 17, App1

28	766	36.0	414	1	US-08-002-202-13 Sequence 13, App1
29	766	36.0	414	2	US-08-481-534-13 Sequence 13, App1
30	765	35.9	414	2	US-08-002-202-19 Sequence 19, App1
31	765	35.9	414	2	US-08-481-534-19 Sequence 19, App1
32	725.5	34.1	414	2	US-09-949-016-8143 Sequence 8143, App
33	709.5	33.3	351	2	US-10-000-489-50 Sequence 50, App1
34	706	33.1	448	2	US-10-104-047-3380 Sequence 3380, App
35	703.5	33.0	423	2	US-09-976-594-19 Sequence 19, App1
36	703.5	33.0	423	2	US-09-919-039-19 Sequence 19, App1
37	703.5	33.0	435	2	US-09-912-628-5 Sequence 5, App1
38	701.5	32.9	415	2	US-09-919-039-390 Sequence 390, App
39	698.5	32.8	419	2	US-09-949-016-11541 Sequence 11541, App
40	698	32.8	422	2	US-09-244-111-8 Sequence 8, App1
41	690.5	32.4	417	2	US-10-012-381A-236 Sequence 236, App
42	690.5	32.4	417	2	US-10-015-389A-236 Sequence 236, App
43	690.5	32.4	417	2	US-10-006-768A-236 Sequence 236, App
44	690.5	32.4	417	2	US-10-015-671A-236 Sequence 236, App
45	690.5	32.4	417	2	US-10-015-393A-236 Sequence 236, App

ALIGNMENTS

```
RESULT 1
US-09-755-665-14
; Sequence 14, Application US/09755665
; Patent No. 660019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tallion, Bruce B.
; APPLICANT: Soderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-755-665-14

Query Match      100.0%; Score 2130; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.7e-197;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MNPTGLAIFLAVLLTVKGLKPSFSPRYKALSEVQWQMAAKELARQNDLGFKL 60
Db      1 MNPTGLAIFLAVLLTVKGLKPSFSPRYKALSEVQWQMAAKELARQNDLGFKL 60
QY      61 KKAAPNPGNITLSPISISTAFSMLCLGAQDSTLDEIKGFNPRKPKERDLEHGFYII 120
Db      61 KKAAPNPGNITLSPISISTAFSMLCLGAQDSTLDEIKGFNPRKPKERDLEHGFYII 120
QY      121 HELTOKTODKLSIGNTLFDORLOPORKFLBQAKPYSAETLTNTFONLEMAOKOINDF 180
Db      121 HELTOKTODKLSIGNTLFDORLOPORKFLBQAKPYSAETLTNTFONLEMAOKOINDF 180
QY      181 ISQKTHKINLLIENIDPGTMLANYIFPRARKHEFPDNTYKEDFLEKNSSVKVP 240
Db      181 ISQKTHKINLLIENIDPGTMLANYIFPRARKHEFPDNTYKEDFLEKNSSVKVP 240
QY      241 MPRSGIYQGYDQKLSCTTLEIPYQKNTAIFLPBEGKLEKLEKLOVDFSRMKTLLS 300
Db      241 MPRSGIYQGYDQKLSCTTLEIPYQKNTAIFLPBEGKLEKLEKLOVDFSRMKTLLS 300
QY      301 RRVVDVSVRLHMTGTFTDKKTLSTYGVSKIPEHGDLTGKIAVHRLKVGAVHKAELKM 360
```


EARLIER APPLICATION NUMBER: 60/090,113
 EARLIER FILING DATE: 1998-06-22
 NUMBER OF SEQ ID NOS: 532
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 134
 LENGTH: 415
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (415)
 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 US-09-461-325-134

Query Match 100.0%; Score 2130; DB 2; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1,7e-197;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVALITVYGLIKPSFSPRNRYKALSEVQGMKQMAKELARQNDLGFRL 60
 DB 1 MNPTGLAIFLAVALITVYGLIKPSFSPRNRYKALSEVQGMKQMAKELARQNDLGFRL 60
 QY 61 KCLAFYNGRNIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFHYII 120
 DB 61 KCLAFYNGRNIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFHYII 120
 QY 121 HELTQKTQDLKLSIGNTLFDORLOPORKFLBDANKFYSAETILTNFQNLMAQKQINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFDORLOPORKFLBDANKFYSAETILTNFQNLMAQKQINDF 180
 QY 181 ISQTHGKINNLLENIDPGVLMLANIIFPRARKHEFDPNVTKEDPFLEKSSVAVPM 240
 DB 181 ISQTHGKINNLLENIDPGVLMLANIIFPRARKHEFDPNVTKEDPFLEKSSVAVPM 240
 QY 241 MFRSGIYQVGYDDKLSCTILIEIPQKNTAIFILPDGSKLHLEKGIQVDFSRWKTLLS 300
 DB 241 MFRSGIYQVGYDDKLSCTILIEIPQKNTAIFILPDGSKLHLEKGIQVDFSRWKTLLS 300
 QY 301 RRVVDVSPRLHMTGTDLKKTLSYIGVSKI FEEHGLDTKIAPRSLKVGSAVKAELKM 360
 DB 301 RRVVDVSPRLHMTGTDLKKTLSYIGVSKI FEEHGLDTKIAPRSLKVGSAVKAELKM 360
 QY 361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIKIVPIGK 414
 DB 361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIKIVPIGK 414

RESULT 5
 US-10-012-542-134
 Sequence 134, Application US/10012542
 Patent No. 6627741
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: 94 Human Secreted Proteins
 FILE REFERENCE: P2029P1
 CURRENT APPLICATION NUMBER: US/10/012,542
 PRIOR FILING DATE: 2001-12-12
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
 NUMBER OF SEQ ID NOS: 532
 SOFTWARE: Patentln Ver. 2.0
 TYPE: PRT

SEQ ID NO 134
 LENGTH: 415
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (415)
 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 US-10-012-542-134

Query Match 100.0%; Score 2130; DB 2; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1,7e-197;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVALITVYGLIKPSFSPRNRYKALSEVQGMKQMAKELARQNDLGFRL 60
 DB 1 MNPTGLAIFLAVALITVYGLIKPSFSPRNRYKALSEVQGMKQMAKELARQNDLGFRL 60
 QY 61 KCLAFYNGRNIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFHYII 120
 DB 61 KCLAFYNGRNIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFHYII 120
 QY 121 HELTQKTQDLKLSIGNTLFDORLOPORKFLBDANKFYSAETILTNFQNLMAQKQINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFDORLOPORKFLBDANKFYSAETILTNFQNLMAQKQINDF 180
 QY 181 ISQTHGKINNLLENIDPGVLMLANIIFPRARKHEFDPNVTKEDPFLEKSSVAVPM 240
 DB 181 ISQTHGKINNLLENIDPGVLMLANIIFPRARKHEFDPNVTKEDPFLEKSSVAVPM 240
 QY 241 MFRSGIYQVGYDDKLSCTILIEIPQKNTAIFILPDGSKLHLEKGIQVDFSRWKTLLS 300
 DB 241 MFRSGIYQVGYDDKLSCTILIEIPQKNTAIFILPDGSKLHLEKGIQVDFSRWKTLLS 300
 QY 301 RRVVDVSPRLHMTGTDLKKTLSYIGVSKI FEEHGLDTKIAPRSLKVGSAVKAELKM 360
 DB 301 RRVVDVSPRLHMTGTDLKKTLSYIGVSKI FEEHGLDTKIAPRSLKVGSAVKAELKM 360
 QY 361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIKIVPIGK 414
 DB 361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIKIVPIGK 414

RESULT 6
 US-10-115-123-134
 Sequence 134, Application US/10115123
 Patent No. 6774216
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: 94 Human Secreted Proteins
 FILE REFERENCE: P202930AP1D2
 CURRENT APPLICATION NUMBER: US/10/115,123
 PRIOR FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: PCT/US99/13418
 PRIOR FILING DATE: 1999-06-15
 PRIOR APPLICATION NUMBER: 60/089,507
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089,508
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089,509
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089,510
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/090,112
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090,113
 PRIOR FILING DATE: 1998-06-22
 NUMBER OF SEQ ID NOS: 532
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 134
 LENGTH: 415
 TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (415)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-115-123-134

Query Match 100.0%; Score 2130; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.7e-197;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPFLGLAIFLAVLLTYKGLLKPSFSPRNKALSEVQGTQMAKELAQNMDLGFKLL 60
DB 1 MNPFLGLAIFLAVLLTYKGLLKPSFSPRNKALSEVQGTQMAKELAQNMDLGFKLL 60
QY 61 KKLAFNPGNITFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
DB 61 KKLAFNPGNITFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
QY 121 HELTQKTDKLSIGNTLFIQRLQPKRFLBDKXNFSYSAETLLTNFQULEMAQKQINDF 180
DB 121 HELTQKTDKLSIGNTLFIQRLQPKRFLBDKXNFSYSAETLLTNFQULEMAQKQINDF 180
QY 181 ISQKTGKINNLIENTDPTWMLLANYIFPRARKHGFDPNVTKEEDFLEKNSVAVPM 240
DB 181 ISQKTGKINNLIENTDPTWMLLANYIFPRARKHGFDPNVTKEEDFLEKNSVAVPM 240
QY 241 MPFSGIYQVGYDDKLSCTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRMKTLIS 300
DB 241 MPFSGIYQVGYDDKLSCTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRMKTLIS 300
QY 301 RRVVDVSVPLHMTGTFDLKKTLSYIGVSKIFEBHGLTKIAPHRSLKVGEAVHAKELKM 360
DB 301 RRVVDVSVPLHMTGTFDLKKTLSYIGVSKIFEBHGLTKIAPHRSLKVGEAVHAKELKM 360
QY 361 DERGTGAAGTGQTPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIG 414
DB 361 DERGTGAAGTGQTPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIG 414

RESULT 7

US-09-755-665-57
Sequence 57, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhidas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tailon, Bruce E.
APPLICANT: Spaderma, Steven K.
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09755,665
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 361
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(361)
OTHER INFORMATION: wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
US-09-755-665-57

Query Match 84.4%; Score 1798; DB 2; Length 361;
Best Local Similarity 96.7%; Pred. No. 1.9e-165;
Matches 349; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 54 DLGFKLLKQLAFNPGNITFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLH 113
DB 1 DLGFKLLKQLAFNPGNITFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLH 60
QY 114 EGFHYIIHETQKTDKLSIGNTLFIQRLQPKRFLBDKXNFSYSAETLLTNFQULEMA 173
DB 61 EGFHYIIHETQKTDKLSIGNTLFIQRLQPKRFLBDKXNFSYSAETLLTNFQULEMA 120
QY 174 QKQINPISQKTHGKINNLIENTDPTWMLLANYIFPRARKHGFDPNVTKEEDFLEKX 233
DB 121 QKQINPISQKTHGKINNLIENTDPTWMLLANYIFPRARKHGFDPNVTKEEDFLEKX 180
QY 234 SSVKVMFMRSGIYQVGYDDKLSCTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFS 293
DB 181 SSVKVMFMRSGIYQVGYDDKLSCTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFS 240
QY 294 RMTLLSRVVDVSVPLHMTGTFDLKKTLSYIGVSKIFEBHGLTKIAPHRSLKVGEAV 353
DB 241 RMTLLSRVVDVSVPLHMTGTFDLKKTLSYIGVSKIFEBHGLTKIAPHRSLKVGEAV 300
QY 354 HRAELKMDERGTGAAGTGQTPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIG 413
DB 301 HRAELKMDERGTGAAGTGQTPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIG 360
QY 414 K 414
DB 361 K 361

RESULT 8

US-10-037-417-66
Sequence 66, Application US/10037417
Patent No. 6903201
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Paturajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine B
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Blierman, Karen
APPLICANT: Malyanar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles B
APPLICANT: Eissen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02

```

1 COUNTRY: USA
2 ZIP: 60606
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Floppy disk
5 COMPUTER: IBM PC compatible
6 OPERATING SYSTEM: PC-DOS/MS-DOS
7 SOFTWARE: Patentin Release #1.0, Version #1.25
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/481,534
10 FILING DATE: 14-SEP-1995
11 CLASSIFICATION: 530
12 ATTORNEY/AGENT INFORMATION:
13 NAME: No. 6022855naa, Kevin E
14 REGISTRATION NUMBER: 35,303
15 REFERENCE/DOCKET NUMBER: 92,448-D
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 312-913-0001
18 TELEFAX: 312-913-0002
19 TELEX:
20 INFORMATION FOR SEQ ID NO: 6:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 394 amino acids
23 TYPE: amino acid
24 TOPOLOGY: linear
25 MOLECULE TYPE: protein
26 US-08-481-534-6
27
28 Query Match 37.5%; Score 798; DB 2; Length 394;
29 Best Local Similarity 43.3%; Pred. No. 1.3e-68;
30 Matches 157; Conservative 72; Mismatches 132; Indels 2; Gaps 1
31
32 QY DLGFKLLKQLAFYNGRNIPLSPISISPAESMLCIGAQDSTLIDIKGFNFR--KMPKED 111
33 DB 32 EFAPSLYRQLAHQNSNTNIFSPSIVATAFAMLSIGTKADTHDILBGLNTFNLNQIPEAQ 91
34
35 QY 112 LHGEFHYIHETLTKTQDDKLSIGENTPLFIDQRLQRPQKFFLEDACKNFSAEITLTFQMLE 171
36 DB 92 IHGEFQELIRLTLPNDPSQLQTLTNGGLFLSGGLVDKFLDVKKLYHSEAFYVFGDTE 151
37
38 QY 172 MAQQLNDFISQKHGKINNLINENIDEGTWLLANVIFFRARWKGEFPDNTKEDFPLE 231
39 DB 152 QAKQINDVYEKGQKIVDLVKELNDYFALVNYIFFKQKMRPREVQDTBEDDFHVD 211
40
41 QY 232 KNSSVKVPVMEFRSGIYGVYDDKLSCTTLEIPIYKNTAIFILPDEGKLKLEKGLQVDT 291
42 DB 212 QVTLVKKVPMKKRLCMFNIHQCKKLSWVLMKKYLGNNATAFFLLDEGKLQHLNBLTHDI 271
43
44 QY 292 FSRWKTLISRVDVSVPLMHTGTPDLTKTSLSYIGVSKIFEEHGDLTFLKAPHSIAKGE 351
45 DB 272 IYKFLNEDRRSASLHPLKSLTGTVDKSVLGGQGITKVPNSGADISGVTEAPLKLKSK 331
46
47 QY 352 AVHKAELKMDERGETGAAGTGAQTLPMETPLVNVIDKPYLLIYSBKIPSVLFLGKIYNP 411
48 DB 332 AVHKAVALTIDKEGTEAAGAFLEAIPMSIIPREYKFNKPEVLEMLQNTKSLFLWQKYNP 391
49
50 QY 412 IKG 414
51 DB 392 TKG 394
52
53 RESULT 10
54 US-08-481-534-11
55 Sequence 11, Application US/08481534
56 Patent No. 6022855
57 GENERAL INFORMATION:
58 APPLICANT: Thomas, Gary
59 APPLICANT: Anderson, Eric D
60 APPLICANT: Thomas, Laurel
61 APPLICANT: Haylick, Joel S
62 APPLICANT: Nelson, Jay
63 APPLICANT: Stenglen, Stephan G
64 TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
65 TITLE OF INVENTION: Endoprotease

```

```

/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
/ STREET: 300 South Wacker Drive
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,534
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6022855nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 92,448-D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 394 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Modified site
/ LOCATION: 355..358
/ OTHER INFORMATION: /label=Variant
/ OTHER INFORMATION: /note="The amino acid sequence is the amino acid
/ OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
/ OTHER INFORMATION: protein, alpha-1-antitrypsin Pittsburgh."
/ US-08-481-534-11

```

```

Query Match 37.2%; Score 792; DB 2; Length 394;
Best Local Similarity 43.0%; Pred. No. 4.8e-68;
Matches 156; Conservative 72; Mismatches 133; Indels 2; Gaps 1;

QY 54 DLGFKLLKLAAYNPGRNIFLSPISSTAFSMCLGAODSTLDEIRKGFNR--KMPKRD 111
DB 32 EFAFSLYRQLAQNSNTNIFSPVSIAINFAMLSLGTAKDTHDELBGINFNLTOIPEAQ 91
QY 112 LHEGFHYIITHELTQTKDLSIGNTLFIQRLQPORFLEDAKNFYSAETIITNFONLE 171
DB 92 IHEGFQELLRLTNQDPDQQLTGTNGLFLSQGLKLVDFKLEDAKLYHSEAFVNFQDTE 151
QY 172 MAQKOINDFISQTHGKINNLINIDPGTWMLANYIFPRARKHEPDPNVTKEEDFPLE 231
DB 152 QAKKOINDYVEKGTQKIVDLVKELDRTVPALVNIIFFGKMERPEVQDTEEDFHYD 211
QY 232 KNSSVKVPMMFSGIYQVGYDDKLSCTIIEIPYOKNITAIFILPDEGKLKHEKGLQVDT 291
DB 212 QYTVVAVPMWKLGMENIQHCKKLSWVLLMKYLGNAIAIFLPDGGKLOHLENELTHDI 271
QY 292 ESRWKTLSRRVVDVSPRLAMTGTDLKKTLSTYGVSKIPEESHGULTIAPRRSLKVEE 351
DB 272 IIRKFLIENEDRRSASLHLPLKLSITGYDLKSVGLQGLITKVFSGADLSGTEBAPLKSK 331
QY 352 AVHKAELKMDERGTEGAAGTGAQTLPMENPLVYKIDKPYILLIYSKISVFLGIQVNP 411
DB 332 AHHKAVLTIDEGKTEAAGMPLAIPRRSLPPEVKENKPFVPLMIEONTYSPLFMGKVNAP 391
QY 412 IGG 414
DB 392 TGG 394

```

```

RESULT 11
US-08-481-534-9
/ Sequence 9; Application US/08481534
/ Patent No. 6022855
/ GENERAL INFORMATION:
/ APPLICANT: Thomas, Gary
/ APPLICANT: Anderson, Eric D
/ APPLICANT: Thomas, Laurel
/ APPLICANT: Hayflick, Joel S
/ APPLICANT: Nelson, Jay
/ APPLICANT: Stenglen, Stephen G
/ TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
/ STREET: 300 South Wacker Drive
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,534
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6022855nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 92,448-D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 394 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Modified site
/ LOCATION: 355..358
/ OTHER INFORMATION: /label=Variant
/ OTHER INFORMATION: /note="The amino acid sequence is the amino acid
/ OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
/ OTHER INFORMATION: protein, alpha-1-antitrypsin Portland."
/ US-08-481-534-9

Query Match 37.1%; Score 791; DB 2; Length 394;
Best Local Similarity 43.0%; Pred. No. 6e-68;
Matches 156; Conservative 72; Mismatches 133; Indels 2; Gaps 1;

QY 54 DLGFKLLKLAAYNPGRNIFLSPISSTAFSMCLGAODSTLDEIRKGFNR--KMPKRD 111
DB 32 EFAFSLYRQLAQNSNTNIFSPVSIAINFAMLSLGTAKDTHDELBGINFNLTOIPEAQ 91
QY 112 LHEGFHYIITHELTQTKDLSIGNTLFIQRLQPORFLEDAKNFYSAETIITNFONLE 171
DB 92 IHEGFQELLRLTNQDPDQQLTGTNGLFLSQGLKLVDFKLEDAKLYHSEAFVNFQDTE 151
QY 172 MAQKOINDFISQTHGKINNLINIDPGTWMLANYIFPRARKHEPDPNVTKEEDFPLE 231
DB 152 QAKKOINDYVEKGTQKIVDLVKELDRTVPALVNIIFFGKMERPEVQDTEEDFHYD 211
QY 212 QYTVVAVPMWKLGMENIQHCKKLSWVLLMKYLGNAIAIFLPDGGKLOHLENELTHDI 271
DB 272 IIRKFLIENEDRRSASLHLPLKLSITGYDLKSVGLQGLITKVFSGADLSGTEBAPLKSK 331
QY 332 AVHKAELKMDERGTEGAAGTGAQTLPMENPLVYKIDKPYILLIYSKISVFLGIQVNP 411
DB 392 TGG 394

```

QY 292 PSNRKTLISRRVVDVSPRLMTGTFDLKTLSYIGVSKIPEEHGDLTKIAPHRSKLVGE 351
Db 272 IYKLEBNDRRSASLHPKLSITGTVDLKSGLGKITKVSNGADLSGVTBEAPLTKSK 331
QY 352 AVHKAELKMDERBTEGAAGTLPMEPTLVYKIDKPYLLIYSEKIPSVLFLGKIVNP 411
Db 332 AVHKAVALTIDKGTGAAGAMFLERIPSPPEVKFNKPFVLMIBONTKSPLEFMGKVVNP 391
QY 412 IKG 414
Db 392 TGR 394

RESULT 12

US-08-002-202-6
; Sequence 6, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Furin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-002-202-6

Query Match 37.1%; Score 790; DB 1; Length 394;

Best Local Similarity 43.0%; Pred. No. 7,5e-68;
Matches 156; Conservative 72; Mismatches 133; Indels 2; Gaps 1;

QY 54 DLGFKLLKLLAFNPGNITPLSISTAFSMLCIGADSTLDEIKGFNR--KMPKED 111
Db 32 BPAFSLYKQLAHOSNSNITPSPVSIATAFAMLSLGTADTHDILBLGNLNLTEIPEAQ 91
QY 112 LHGEFYIHELTOKTQDLKLSIGNTLFIQRLQPKRKFLEDAKNFYSAEITILTFONLE 171
Db 92 IHGFGQELATLNOQPSQLTLTGNGFLSGQLKLVDFLEDEVKLYHSAFAFVNPEDTE 151
QY 172 MAOKQINDPISQTHGKINNLIENIDPGTMLLANIYFPAARKHEEDPVVYKEEDFLE 231
Db 152 QAKQKQINDVYKGTGKIVDLVKELDRDTVFALVNIYFFGKWBKRPPEVVDTESEDPHVD 211

QY 232 KNSGVKVPMPFRSGIYGVYDDKLSCTILIEIPYOKNTAIFILPDESKLRLKELQVDT 291
Db 212 QVTTVAVPMKRLGMPNIGQCKKLSVNLMTKLGNATLFFLPDEBKQHLNHELTHDI 271
QY 292 PSNRKTLISRRVVDVSPRLMTGTFDLKTLSYIGVSKIPEEHGDLTKIAPHRSKLVGE 351
Db 272 IYKLEBNDRRSASLHPKLSITGTVDLKSGLGKITKVSNGADLSGVTBEAPLTKSK 331
QY 352 AVHKAELKMDERBTEGAAGTLPMEPTLVYKIDKPYLLIYSEKIPSVLFLGKIVNP 411
Db 332 AVHKAVALTIDKGTGAAGAMFLERIPSPPEVKFNKPFVLMIBONTKSPLEFMGKVVNP 391
QY 412 IKG 414
Db 392 TGR 394

RESULT 13

US-08-553-488A-1
; Sequence 1, Application US/08553488A
; Patent No. 5817484
; GENERAL INFORMATION:
; APPLICANT: YU, Myeong-Hee
; APPLICANT: KWON, Ki-Sun
; APPLICANT: LEE, Kee-Nyung
; APPLICANT: SHIN, Hwa-Soo
; TITLE OF INVENTION: THERMORESISTANT ALPHA-1-ANTITRYPSIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: YU, Myeong-Hee
; STREET: 3-1003, Hankang Apartment, 49-8, Jjamwon-dong,
; STREET: Secho-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 137-030
; ADDRESSEE: KWON, Ki-Sun
; STREET: 130-1306, Hanbit Apartment, Oun-dong,
; STREET: Yuseong-gu
; CITY: Taejeon
; STATE: Taejeon
; COUNTRY: Republic of Korea
; ZIP: 305-333
; ADDRESSEE: SHIN, Hwa-Soo
; STREET: 3-303, Sindonga Apartment, Yongjeon-dong,
; STREET: Dong-gu
; CITY: Taejeon
; STATE: Taejeon
; COUNTRY: Republic of Korea
; ZIP: 300-200
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,488A
; FILING DATE: 20-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 93-8510
; FILING DATE: 18-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
OTHER INFORMATION: wild type human '-1-antitrypsin
US-08-553-488A-1

Query Match 37.1%; Score 790; DB 1; Length 394;
Best Local Similarity 42.7%; Pred. No. 7,5e-68;
Matches 155; Conservative 74; Mismatches 132; Indels 2; Gaps 1;

QY 54 DLGFKLLKLAFAVNPGRNIFLSPISISTAFSMCLGAQDSTLDEIKQGFNR--KMEKD 111
DB 32 EFAPSLYRQLAHOSNSTNIFSPVSITAFAMLSVGTAKDTHDEILGELNLTETIPQAQ 91
QY 112 LHGPFYIHELTKQTKDLSIGNTLFIDRLQPKFLEDAKNFYSAETILTNQNTL 171
DB 92 IHGFGDELHTLTPQPSQLQTLTGNGLFLSEGLVDKFLBDVKLVHSAFTVNFQDTE 151
QY 172 MAQKQINDFISQTHGKINNLEINIDPGYMLLANTYIFFRARKHEFDPVNTKEEDFFLE 231
DB 152 EAKKQINNVEKKTQKGVVDLVKELDRDVFALVNIFFPKGWERPFVEATEEEDFHVD 211
QY 232 KNSVAVPMFRSGIYOVGDLSCTIIEIPYQKNTAIFILPDGKLNLEKGLQVDT 291
DB 212 QATTVAVPMFRKLGMPNIOHCKLSSWVLMKYLGNATAIFFLPDGGKQLHLENELTHDI 271
QY 292 FSRWKTLLSRVVDVSPRLHMTGTPDLKKTLSYIGVSKI FEEHGDLTAKIAPHRSIKVGE 351
DB 272 ITFPLENERRRANLHLPKLAITGTVDLKTIVGHLGDTKVFSGADLSGVTEDAPLKLK 330
QY 352 AVHKAELKNDERGTGSAAGTQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKI VNP 411
DB 332 AVHKAVALTIDKGTGAAGAMFLAIPMSIPPEVKFNPVFLMIDQNTKSPLEFGK VNP 391
QY 412 IGR 414
DB 392 TQK 394

RESULT 14
US-09-755-665-58
Sequence 58, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tailion, Bruce E.
APPLICANT: Spaderma, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 363
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-58

Query Match 36.9%; Score 785; DB 2; Length 363;

Best Local Similarity 41.6%; Pred. No. 2e-67;
Matches 151; Conservative 83; Mismatches 127; Indels 2; Gaps 1;

QY 54 DLGFKLLKLAFAVNPGRNIFLSPISISTAFSMCLGAQDSTLDEIKQGFNR--KMEKD 111
DB 1 EFAPSLYRQLAHOSNSTNIFSPVSITAFAMLSVGTAKDTHDEILGELNLTETIPQAQ 60
QY 112 LHGPFYIHELTKQTKDLSIGNTLFIDRLQPKFLEDAKNFYSAETILTNQNTL 171
DB 61 VHGFGDELHTLTPQPSQLQTLTGNGLFLKSLKVDKFLBDVKLVHSAFTVNFQDTE 120
QY 172 MAQKQINDFISQTHGKINNLEINIDPGYMLLANTYIFFRARKHEFDPVNTKEEDFFLE 231
DB 121 EAKKQINNVEKKTQKGVVDLVKELDRDVFALVNIFFPKGWERPFVEATEEEDFHVD 180
QY 232 KNSVAVPMFRSGIYOVGDLSCTIIEIPYQKNTAIFILPDGKLNLEKGLQVDT 291
DB 181 QATTVAVPMFRKLGMPNIOHCKLSSWVLMKYLGNATAIFFLPDGGKQLHLENELTHDI 240
QY 292 FSRWKTLLSRVVDVSPRLHMTGTPDLKKTLSYIGVSKI FEEHGDLTAKIAPHRSIKVGE 351
DB 241 ITFPLENERRRANLHLPKLAITGTVDLKTIVGHLGDTKVFSGADLSGVTEDAPLKLK 300
QY 352 AVHKAELKNDERGTGSAAGTQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKI VNP 411
DB 301 AVHKAVALTIDKGTGAAGAMFLAIPMSIPPEVKFNPVFLMIDQNTKSPLEFGK VNP 360
QY 412 IGR 414
DB 361 TQK 363

RESULT 15
US-09-023-339-1
Sequence 1, Application US/09023339
Patent No. 6127145
GENERAL INFORMATION:
APPLICANT: Sutcliffe, Thomas D.
APPLICANT: Rodriguez, Raymond L.
TITLE OF INVENTION: Production of '-1-Antitrypsin
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,339
FILING DATE: 13-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,991
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Petichory, Joanne R
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 0665-0003.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

THIS PAGE BLANK (USPTO)

Db 301 REVVDVSVPRHMTGTDFDKLTSLTYGSKIFEHGDLTAKIAPHRSLSKGEAVHAKALKM 360
 Qy 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKIIVNPIGK 414
 Db 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKIIVNPIGK 414

RESULT 2

US-09-755-665-55
 ; Sequence 55, Application US/09755665
 ; Patent No. 6600019
 ; GENERAL INFORMATION:
 ; APPLICANT: Prayaga, Sudhidas K.
 ; APPLICANT: Majumder, K. K.
 ; APPLICANT: Tailon, Bruce E.
 ; APPLICANT: Spaderna, Steven K.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: MacDougall, John
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 15966-631
 ; CURRENT APPLICATION NUMBER: US/09/755,665
 ; CURRENT FILING DATE: 2001-08-14
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
 ; PRIOR FILING DATE: 2000-01-06
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 55
 ; LENGTH: 414
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-755-665-55

Query Match 100.0%; Score 2130; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 1,7e-197;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPTGLAIFLAVALITVKGILKPSFSPRNRYKALSEVQGMKORMAKELARQNDLGFKLL 60
 Db 1 MNPTGLAIFLAVALITVKGILKPSFSPRNRYKALSEVQGMKORMAKELARQNDLGFKLL 60
 Qy 61 KCLAFYNGRNIPLSPISISTAFSMLCLGAODSTLDEIKGFFNRKMBEKLHGFHYII 120
 Db 61 KCLAFYNGRNIPLSPISISTAFSMLCLGAODSTLDEIKGFFNRKMBEKLHGFHYII 120
 Qy 121 HELTQKODKLSTIGNTLFDORLQPORKEFLDANKFYSAETILTNPONLEMAOKQINDF 180
 Db 121 HELTQKODKLSTIGNTLFDORLQPORKEFLDANKFYSAETILTNPONLEMAOKQINDF 180
 Qy 181 ISQTHGKINLLIENIDPGTVMLLANYIFPRARKHEFDPNVTKEDFLEKNSSVKVP 240
 Db 181 ISQTHGKINLLIENIDPGTVMLLANYIFPRARKHEFDPNVTKEDFLEKNSSVKVP 240
 Qy 241 MFRSGIYGVGDYDDKLTSTLIEIPYOKNITAFILPDGSKLHLEKGLQVDFFSRWKTLIS 300
 Db 241 MFRSGIYGVGDYDDKLTSTLIEIPYOKNITAFILPDGSKLHLEKGLQVDFFSRWKTLIS 300
 Qy 301 RRVVDVSVPRHMTGTDFDKLTSLTYGSKIFEHGDLTAKIAPHRSLSKGEAVHAKALKM 360
 Db 301 RRVVDVSVPRHMTGTDFDKLTSLTYGSKIFEHGDLTAKIAPHRSLSKGEAVHAKALKM 360
 Qy 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKIIVNPIGK 414
 Db 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKIIVNPIGK 414

RESULT 3
 US-09-755-665-56
 ; Sequence 56, Application US/09755665
 ; Patent No. 6600019
 ; GENERAL INFORMATION:
 ; APPLICANT: Prayaga, Sudhidas K.
 ; APPLICANT: Majumder, K. K.

NOVX polypeptides
 re productive
 abnormal malfunctions
 endocrinological defects
 pathologic spermatogenesis

APPLICANT: Tailon, Bruce E.
 APPLICANT: Spaderna, Steven K.
 APPLICANT: Spytek, Kimberly A.
 APPLICANT: MacDougall, John
 TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 15966-631
 CURRENT APPLICATION NUMBER: US/09/755,665
 CURRENT FILING DATE: 2001-08-14
 PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
 PRIOR FILING DATE: 2000-01-06
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 56
 LENGTH: 414
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-755-665-56

Query Match 100.0%; Score 2130; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 1,7e-197;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPTGLAIFLAVALITVKGILKPSFSPRNRYKALSEVQGMKORMAKELARQNDLGFKLL 60
 Db 1 MNPTGLAIFLAVALITVKGILKPSFSPRNRYKALSEVQGMKORMAKELARQNDLGFKLL 60
 Qy 61 KCLAFYNGRNIPLSPISISTAFSMLCLGAODSTLDEIKGFFNRKMBEKLHGFHYII 120
 Db 61 KCLAFYNGRNIPLSPISISTAFSMLCLGAODSTLDEIKGFFNRKMBEKLHGFHYII 120
 Qy 121 HELTQKODKLSTIGNTLFDORLQPORKEFLDANKFYSAETILTNPONLEMAOKQINDF 180
 Db 121 HELTQKODKLSTIGNTLFDORLQPORKEFLDANKFYSAETILTNPONLEMAOKQINDF 180
 Qy 181 ISQTHGKINLLIENIDPGTVMLLANYIFPRARKHEFDPNVTKEDFLEKNSSVKVP 240
 Db 181 ISQTHGKINLLIENIDPGTVMLLANYIFPRARKHEFDPNVTKEDFLEKNSSVKVP 240
 Qy 241 MFRSGIYGVGDYDDKLTSTLIEIPYOKNITAFILPDGSKLHLEKGLQVDFFSRWKTLIS 300
 Db 241 MFRSGIYGVGDYDDKLTSTLIEIPYOKNITAFILPDGSKLHLEKGLQVDFFSRWKTLIS 300
 Qy 301 RRVVDVSVPRHMTGTDFDKLTSLTYGSKIFEHGDLTAKIAPHRSLSKGEAVHAKALKM 360
 Db 301 RRVVDVSVPRHMTGTDFDKLTSLTYGSKIFEHGDLTAKIAPHRSLSKGEAVHAKALKM 360
 Qy 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKIIVNPIGK 414
 Db 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKIIVNPIGK 414

RESULT 4
 US-09-461-325-134
 ; Sequence 134, Application US/09461325A
 ; Patent No. 6475753
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 94 Human Secreted Proteins
 ; FILE REFERENCE: P2029P1
 ; CURRENT APPLICATION NUMBER: US/09/461,325A
 ; CURRENT FILING DATE: 1999-12-14
 ; EARLIER APPLICATION NUMBER: PCT/US99/13418
 ; EARLIER FILING DATE: 1999-06-15
 ; EARLIER APPLICATION NUMBER: 60/089,507
 ; EARLIER FILING DATE: 1998-06-16
 ; EARLIER APPLICATION NUMBER: 60/089,508
 ; EARLIER FILING DATE: 1998-06-16
 ; EARLIER APPLICATION NUMBER: 60/089,509
 ; EARLIER FILING DATE: 1998-06-16
 ; EARLIER APPLICATION NUMBER: 60/089,510
 ; EARLIER FILING DATE: 1998-06-16
 ; EARLIER APPLICATION NUMBER: 60/090,112
 ; EARLIER FILING DATE: 1998-06-22

THIS PAGE BLANK (USPTO)

PS Claim 1, Page 32, 144pp; English.

XX The invention relates to nucleic acids encoding NOVX (X being an integer
 CC from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
 CC useful in diagnosing, treating or manufacturing a medicament for a
 CC disease or disorder associated with NOVX e.g. cell proliferation (cancer
 CC and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
 CC disorders (e.g. of spermatogenesis), haematopoietic, immunological,
 CC inflammatory and tumour related disorders, emphysema, cirrhosis, wound
 CC healing. NOVX nucleic acids are also useful in gene therapy. They are
 CC also used for screening for a modulator of activity or of latency or
 CC predisposition to a NOVX-associated disorder. They are also useful for
 CC determining the presence of or predisposition to a NOVX-associated
 CC disorder. The present sequence represents NOV7 (Ab132990 B), which has
 CC sequence homology to an unidentified human secreted protein (HMHGUS54)
 CC and to alpha anti-trypsin

XX Sequence 414 AA;

SO

Query Match 100.0%; Score 2130; DB 4; Length 414;
 Best Local Similarity 100.0%; Pred. No. 4.4e-181;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTLGAIPLAVLITVKGILKPSFSPRYKALSEVQGMKQMAAKELARQNDLGFKLL 60
 DB 1 MNPTLGAIPLAVLITVKGILKPSFSPRYKALSEVQGMKQMAAKELARQNDLGFKLL 60

QY 61 KKLAFNPGRNITFLSPISITAFSMLCLGAQDSTLDEIKQGFNPRKPEKDLHEGFHYII 120
 DB 61 KKLAFNPGRNITFLSPISITAFSMLCLGAQDSTLDEIKQGFNPRKPEKDLHEGFHYII 120

QY 121 HELTQKTQDLKLSIGNTLFIQDRLOPQRKFLBDARNFYSAEITLTNFOULEMAQKQINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFIQDRLOPQRKFLBDARNFYSAEITLTNFOULEMAQKQINDF 180

QY 181 ISQKTHGKINNIENIDPGTVMLANIYFFRARKWHEPDNVTKEEDFLEKNSSVKVPVM 240
 DB 181 ISQKTHGKINNIENIDPGTVMLANIYFFRARKWHEPDNVTKEEDFLEKNSSVKVPVM 240

QY 241 MFRSGIYGVGYDDKLSCTTILEIPYQKNITAIFFILPDEGKHLKELQVDTFSRWKTLIS 300
 DB 241 MFRSGIYGVGYDDKLSCTTILEIPYQKNITAIFFILPDEGKHLKELQVDTFSRWKTLIS 300

QY 301 RRVADVSVPLRMTGTFDLKKTLISYGVSKIPEHSGDLTKIAPHRSLKVGSAVHKAELKX 360
 DB 301 RRVADVSVPLRMTGTFDLKKTLISYGVSKIPEHSGDLTKIAPHRSLKVGSAVHKAELKX 360

QY 361 DERGTGAGCTGAGTIPMERPLVVKIDKPYLLIYSEKISYVFLGKIYVPIGK 414
 DB 361 DERGTGAGCTGAGTIPMERPLVVKIDKPYLLIYSEKISYVFLGKIYVPIGK 414

DB 361 DERGTGAGCTGAGTIPMERPLVVKIDKPYLLIYSEKISYVFLGKIYVPIGK 414

RESULT 2
 AAE04885
 ID AAE04885 standard; protein; 414 AA.
 XX
 AC AAE04885;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human protease protein-12 (PRTS-12).
 XX
 XX Human; protease protein-12; PRTS-12; cytostatic; hypotensive; antiviral;
 KW gastroenteric disorder; anorexia; dysphagia; cardiovascular disorder;
 KW atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;
 KW Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;
 KW acquired immune deficiency syndrome; AIDS; neurological disorder; aetna;
 KW developmental disorder; epithelial disorder; eczema; dementia; noctropic;
 KW neurological disorder; reproductive disorder; infertility; teratogenesis;
 KW immunosuppressive; drug screening; actinic keratosis; cardiac; epilepsy;
 KW anaemia; antitumour; gene therapy; antibacterial.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..19
 FT Peptide /label= Signal_peptide
 FT Protein 20..414
 FT /note= "Mature human PRTS-12"

XX WO200146443-A2.
 XX
 XX 28-JUN-2001.
 XX
 XX 19-DEC-2000; 2000MO-US034811.
 XX
 XX 23-DEC-1999; 99US-0172055P.
 XX 21-JAN-2000; 2000US-0177334P.
 XX 28-JAN-2000; 2000US-0178884P.
 XX 02-FEB-2000; 2000US-0179903P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Yang J, Baughn MR, Burford N, Au-Young J, Lu DM, Reddy R;
 PI Yue H, Nguyen DB, Tang YT, Yao MG, Lai P;
 XX WPI; 2001-410880/44.
 XX N-PSDB; AAD09549.
 XX
 XX Novel human protease proteins (PRTS) useful for diagnosing, treating,
 PT preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
 PT cell proliferative disorders associated with abnormal expression of PRTS.
 XX
 PS Claim 1, Page 118, 129pp; English.

XX The present sequence is human protease protein (PRTS-12). Human PRTS and
 CC its nucleic acid molecule are useful for the diagnosis, treatment and
 CC prevention of disorders associated with increased or decreased expression
 CC of PRTS. Examples of such disorders include, gastrointestinal disorder
 CC such as anorexia, dysphagia; cardiovascular disorder such as
 CC atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as
 CC acquired immune deficiency syndrome (AIDS), asthma; cell proliferative
 CC disorder such as actinic keratosis, cirrhosis; developmental disorder
 CC such as epilepsy, anaemia; epithelial disorder such as allergic contact
 CC dermatitis, eczema; neurological disorder such as Alzheimer's disease,
 CC dementia and reproductive disorder such as infertility and teratogenesis.
 CC PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or
 CC transgenic animals (mice or rats) to model human disease. PRTS DNA is
 CC also in useful in gene therapy. PRTS and its immunogenic fragments are
 CC useful for screening libraries of compounds in several drug screening
 CC assays. PRTS is useful for analysing the proteome of a tissue or cell
 CC type

XX Sequence 414 AA;

SO

Query Match 100.0%; Score 2130; DB 4; Length 414;
 Best Local Similarity 100.0%; Pred. No. 4.4e-181;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTLGAIPLAVLITVKGILKPSFSPRYKALSEVQGMKQMAAKELARQNDLGFKLL 60
 DB 1 MNPTLGAIPLAVLITVKGILKPSFSPRYKALSEVQGMKQMAAKELARQNDLGFKLL 60

QY 61 KKLAFNPGRNITFLSPISITAFSMLCLGAQDSTLDEIKQGFNPRKPEKDLHEGFHYII 120
 DB 61 KKLAFNPGRNITFLSPISITAFSMLCLGAQDSTLDEIKQGFNPRKPEKDLHEGFHYII 120

QY 121 HELTQKTQDLKLSIGNTLFIQDRLOPQRKFLBDARNFYSAEITLTNFOULEMAQKQINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFIQDRLOPQRKFLBDARNFYSAEITLTNFOULEMAQKQINDF 180

QY 181 ISQKTHGKINNIENIDPGTVMLANIYFFRARKWHEPDNVTKEEDFLEKNSSVKVPVM 240
 DB 181 ISQKTHGKINNIENIDPGTVMLANIYFFRARKWHEPDNVTKEEDFLEKNSSVKVPVM 240

QY 241 MFRSGIYGVGYDDKLSCTTILEIPYQKNITAIFFILPDEGKHLKELQVDTFSRWKTLIS 300

```

Db      241 MFRSGIYQVGDYDKLSTIIIEIPYQKNITAIIFILPDEGKLHLEKGLQVDTFSWKTLIS 300
Qy      301 RRVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPRSLKVGSAVHKAELKM 360
Db      301 RRVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPRSLKVGSAVHKAELKM 360
Qy      361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 414
Db      361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 414

RESULT 3
ADA57300
ID      ADA57300 standard; protein; 414 AA.
XX
AC      ADA57300;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Human secreted protein #583.
XX
KW      immunosuppressive; antiinflammatory; antiaesthetic; antiallergic;
KW      cyclostatic; cerebroprotective; neuroprotective; nootropic;
KW      cardiovascular; antiarteriosclerotic; gene therapy;
KW      human secreted protein; immune disorder; neurodegenerative disorders;
KW      respiratory disorder; cancer; CNS disorder; inflammation;
KW      inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW      multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW      Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW      triple helix formation; antisense gene therapy; forensic biology.
XX
OS      Homo sapiens.
XX
PN      W02002102994-A2.
XX
PD      27-DEC-2002.
XX
PF      19-MAR-2002; 2002WC-US008278.
XX
PR      21-MAR-2001; 2001US-0277340P.
PR      19-JUL-2001; 2001US-0306171P.
PR      13-NOV-2001; 2001US-031287P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Rosen CA, Ruben SM;
XX
DR      WPI; 2003-167512/16.
DR      N-PSDB; ADA56404.
XX
PT      New human secreted polypeptides and polynucleotides, useful for
PT      diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT      conditions, respiratory disorders, cancers, CNS disorders, or
PT      neurodegenerative disorders.
XX
PS      Claim 13; SEQ ID NO 1490; 1754bp; English.
XX
CC      The invention relates to 592 new human secreted polypeptides useful for
CC      diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC      conditions, respiratory disorders, cancers, CNS disorders, or
CC      neurodegenerative disorders, or polypeptides comprising an amino acid
CC      sequence at least 95% identical to the new sequences. The polypeptides,
CC      antibodies or antibody fragments that bind to the polypeptides, nucleic
CC      acids encoding the polypeptides, agonists or antagonists that binds to
CC      the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC      compositions for diagnosing, treating or preventing an e.g. immune
CC      disorder, inflammatory conditions (e.g. inflammatory bowel disease,
CC      nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC      allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC      (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC      disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC      cardiovascular disorders (e.g. atherosclerosis or myocarditis). The

```

```

CC      polynucleotides are useful for chromosome identification, chromosome
CC      mapping, for controlling gene expression through triple helix formation
CC      or antisense DNA or RNA, in gene therapy, for identifying individuals
CC      from minute biological samples, in forensic biology, and as hybridization
CC      probes. The polypeptides are useful for as molecular weight markers on
CC      sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC      gels, to raise antibodies, for testing biological activities, and for
CC      treating or preventing neural disorders, immune system disorders,
CC      muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC      renal, proliferative and/or cancerous diseases. This sequence corresponds
CC      to one of the polypeptide of the invention. Note: The sequence data for
CC      this patent did form part of the printed specification, but was obtained
CC      in electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences.
XX
SQ      Sequence 414 AA;
XX
Query Match      100.0%; Score 2130; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 4,4e-181;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MNPTGLAIFLAVALITTKGLKSPSPRYKALSEVQGWQRMAAKELARQNDLGRKL 60
Db      1 MNPTGLAIFLAVALITTKGLKSPSPRYKALSEVQGWQRMAAKELARQNDLGRKL 60
Qy      61 KGLAFVYRGNIFLSPISISTAFSMLCTGAQDSTLDEIKQGFNRKMPERDLHGFHYII 120
Db      61 KGLAFVYRGNIFLSPISISTAFSMLCTGAQDSTLDEIKQGFNRKMPERDLHGFHYII 120
Qy      121 HELTOKTQDLKLSIGNTLFIIDRLQPORKELEDAKNFYSAEITLTNPNLEMAQKQINDF 180
Db      121 HELTOKTQDLKLSIGNTLFIIDRLQPORKELEDAKNFYSAEITLTNPNLEMAQKQINDF 180
Qy      181 ISQKTHGKINNLLENIDPGVYMLANYIFPRAWKHFPDENVYKSEDFLEKSSVYVPM 240
Db      181 ISQKTHGKINNLLENIDPGVYMLANYIFPRAWKHFPDENVYKSEDFLEKSSVYVPM 240
Qy      241 MFRSGIYQVGDYDKLSTIIIEIPYQKNITAIIFILPDEGKLHLEKGLQVDTFSWKTLIS 300
Db      241 MFRSGIYQVGDYDKLSTIIIEIPYQKNITAIIFILPDEGKLHLEKGLQVDTFSWKTLIS 300
Qy      301 RRVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPRSLKVGSAVHKAELKM 360
Db      301 RRVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPRSLKVGSAVHKAELKM 360
Qy      361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 414
Db      361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 414

RESULT 4
ADA41179
ID      ADA41179 standard; protein; 414 AA.
XX
AC      ADA41179;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Human secreted protein.
XX
KW      Human, secreted protein; cancer; hyperproliferative disorder;
KW      rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW      anaemia; allergic reaction; asthma; cardiovascular disorder;
KW      wound healing; cyclostatic; immunosuppressive; nootropic; neuroprotective;
KW      antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW      vulnerary; cardiac; gene therapy.
XX
OS      Homo sapiens.
XX
PN      W02002102993-A2.
XX
PD      27-DEC-2002.
XX

```


QY 241 MFRSGIYQVGYDDKLSCTILEIPIYQKNITAIPIIPDESKLKHLEKGLQVDFSRWKTLLS 300
 DB 241 MFRSGIYQVGYDDKLSCTILEIPIYQKNITAIPIIPDESKLKHLEKGLQVDFSRWKTLLS 300
 QY 301 RRVVDVSVPLHMTGTPTDKTLLSYIGVSKIPEEHGDLTKIAPRSLKVGSAVHKAEIKM 360
 DB 301 RRVVDVSVPLHMTGTPTDKTLLSYIGVSKIPEEHGDLTKIAPRSLKVGSAVHKAEIKM 360
 QY 361 DERGTGAAGTGAOTLPMEPTLVVVKIDKPYLLLIYSEKIPSVLFLGKIIVNPICK 414
 DB 361 DERGTGAAGTGAOTLPMEPTLVVVKIDKPYLLLIYSEKIPSVLFLGKIIVNPICK 414

RESULT 6
 AAY86217
 ID AAY86217 standard; protein; 415 AA.
 AC AAY86217;
 XX
 DT 19-APR-2000 (first entry)
 XX
 DE Human secreted protein HMGU54, SEQ ID NO:132.
 XX
 KM Human; secreted protein; cancer; tumour; developmental abnormality;
 KM foetal deficiency; blood disorder; immune system disorder; inflammation;
 KM autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KM schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KM atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KM digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KM therapy.
 XX
 KM Homo sapiens.
 XX OS
 PN MO9966041-A1.
 XX
 PD 23-DEC-1999.
 XX
 PF 15-JUN-1999; 99WO-US013418.
 XX
 PR 16-JUN-1998; 98US-0089507P.
 PR 16-JUN-1998; 98US-0089508P.
 PR 16-JUN-1998; 98US-0089509P.
 PR 16-JUN-1998; 98US-0089510P.
 PR 22-JUN-1998; 98US-0090112P.
 PR 22-JUN-1998; 98US-0090113P.
 XX
 PA (HUMA-) HUMAN GENOME SCT INC.
 XX
 PI Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA;
 PI Soppet DR, Brewer LA, Endress GA, Carter KC, Muceneki M, Ebner R;
 PI Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsu G;
 XX
 DR WPI, 2000-106100/09.
 DR N-PSDB; AAZ97021.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 XX
 PS Claim 1; Page 389-390; 586pp; English.
 XX
 CC AA297019 to AA297137 represent 94 isolated human secreted protein genes.
 CC AAY86215 to AAY86333 are the secreted proteins encoded by the 94 human
 CC genes. This sequence represents a fragment of one of the human secreted
 CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions, e.g.,
 CC by protein or gene therapy. Also pathological conditions can be diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new genes. Specific uses are
 CC described for each of the 94 genes, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, tumours, developmental abnormalities and foetal

CC deficiencies, blood disorders, diseases of the immune system, autoimmune
 CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
 CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
 CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
 CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
 CC also useful for identifying their binding partners. The sequences shown
 CC in AAY86334 to AAY86585 represent fragments of the secreted proteins
 XX
 SO Sequence 415 AA;
 QY Query Match 100.0%; Score 2130; DB 3; Length 415;
 DB Best Local Similarity 100.0%; Pred. No. 4,4e-181;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNPTLGAIPLAVLLTVYKGLKPSPPRNKALSEVQGMQRMAKELARQNMGLGFTLL 60
 DB 1 MNPTLGAIPLAVLLTVYKGLKPSPPRNKALSEVQGMQRMAKELARQNMGLGFTLL 60
 QY 61 KGLAFVNPGRNIFLSPISISTAFSMLCLGADSTLDEIKQFNPRAKPEKOLHGFHYII 120
 DB 61 KGLAFVNPGRNIFLSPISISTAFSMLCLGADSTLDEIKQFNPRAKPEKOLHGFHYII 120
 QY 121 HELTQKTQDLKLSIGNTLFIIDQRLQPKFLEDAKNFYSABTILTNFQNLMAQKQINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFIIDQRLQPKFLEDAKNFYSABTILTNFQNLMAQKQINDF 180
 QY 181 ISOQTHKIKINLLENIDPGVMLANIIFPRAKHEFPDPVYKEBDFLEKSSVYVPM 240
 DB 181 ISOQTHKIKINLLENIDPGVMLANIIFPRAKHEFPDPVYKEBDFLEKSSVYVPM 240
 QY 241 MFRSGIYQVGYDDKLSCTILEIPIYQKNITAIPIIPDESKLKHLEKGLQVDFSRWKTLLS 300
 DB 241 MFRSGIYQVGYDDKLSCTILEIPIYQKNITAIPIIPDESKLKHLEKGLQVDFSRWKTLLS 300
 QY 301 RRVVDVSVPLHMTGTPTDKTLLSYIGVSKIPEEHGDLTKIAPRSLKVGSAVHKAEIKM 360
 DB 301 RRVVDVSVPLHMTGTPTDKTLLSYIGVSKIPEEHGDLTKIAPRSLKVGSAVHKAEIKM 360
 QY 361 DERGTGAAGTGAOTLPMEPTLVVVKIDKPYLLLIYSEKIPSVLFLGKIIVNPICK 414
 DB 361 DERGTGAAGTGAOTLPMEPTLVVVKIDKPYLLLIYSEKIPSVLFLGKIIVNPICK 414

RESULT 7
 ABO53360
 ID ABO53360 standard; protein; 415 AA.
 XX
 AC ABO53360;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Novel human secreted protein #3.
 XX
 KM Human; vaccine; immune system disorder; haematopoietic cell disorder;
 KM cancer; autoimmune disorder; rheumatoid arthritis; glomerulonephritis;
 KM HIV infection; anaemia; thrombocytopenia blood coagulation disorder;
 KM blood platelet disorder; wound; heart attack; myocardial infarction;
 KM stroke; scarring; asthma; graft-versus host rejection; inflammation;
 KM hyperproliferative disorder; lymphoproliferative disorder; arthralgia;
 KM aberrant cellular division; cell proliferative disorder; angiogenesis;
 KM cardiovascular disorder; pulmonary heart disease; neovascularisation;
 KM hypertrophic scar; keloid; ocular disorder; diabetic retinopathy;
 KM uveitis; epithelial cell proliferation; neurological disease; apoplexia;
 KM Parkinson's disease; Alzheimer's disease; Huntington's chorea; AIDS;
 KM amyotrophic lateral sclerosis; toxin induced liver disease; septic shock;
 KM cachexia; anorexia; lung damage; infection.
 XX
 OS Homo sapiens.
 XX
 PN US2003065151-A1.
 XX
 PD 03-APR-2003.

PF 04-APR-2002; 2002US-00115123.
 XX 16-JUN-1998; 98US-0089507P.
 PR 16-JUN-1998; 98US-0089508P.
 PR 16-JUN-1998; 98US-0089509P.
 PR 16-JUN-1998; 98US-0089510P.
 PR 22-JUN-1998; 98US-0090112P.
 PR 22-JUN-1998; 98US-0090113P.
 PR 15-JUN-1999; 99MO-US013418.
 PR 14-DEC-1999; 99US-00461325.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Ruben SM, Ni J, Rosen CA, Wei Y, Young P, Florence K, Soppet DR,
 PI Brewer LA, Endress GA, Carter KC, MucenSKI M, Ebner R, Lafleur DW,
 PI Olsen H, Shi Y, Moore PA, Komatseville G;
 XX
 DR MPI; 2003-531736/50.
 DR N-PSDB; ACH66650.
 XX
 PT Novel antibody that binds specifically to a HCEJ069 protein, useful for
 PT detecting the presence of a protein in a biological sample, and for
 PT treating cancers, autoimmune disorders and HIV infection.
 PS
 PS Disclosure; SEQ ID NO 134; 176bp; English.
 XX
 CC The invention relates to an isolated antibody or its fragment that
 CC specifically binds to a protein. The antibody is useful for detecting a
 CC protein in a biological sample, by contacting the biological sample with
 CC the antibody or its fragment and detecting the protein in the biological
 CC sample. The antibody is useful for purifying, detecting and targeting the
 CC human secreted proteins, including both in vitro and in vivo diagnostic
 CC and therapeutic methods. The antibody is useful for immunophenotyping of
 CC cell lines in biological samples and in antibody-based therapies for
 CC treating, inhibiting and preventing diseases, disorders or conditions
 CC associated with aberrant expression and/or activity of the above
 CC proteins. The antibody is useful for treating deficiencies or disorders
 CC of immune system and hematopoietic cells, for increasing differentiation
 CC and proliferation of haematopoietic cells, for treating immune
 CC deficiencies or disorders e.g. cancers, autoimmune disorders (such as
 CC rheumatoid arthritis and glomerulonephritis), HIV infection, anaemia and
 CC thrombocytopenia and as a marker for a particular immune system disease
 CC or disorder. The antibody is also useful for treating blood coagulation
 CC disorders, blood platelet disorders, wounds, heart attacks (infarction),
 CC strokes, scarring and asthma. The antibody is also useful for treating or
 CC preventing graft-versus host rejection, for modulating inflammation, for
 CC treating hyperproliferative disorders e.g. lymphoproliferative disorders
 CC and cancers, for inhibiting aberrant cellular division and for treating
 CC cell proliferative disorders. The antibody is also useful for treating
 CC cardiovascular disorders e.g. pulmonary heart disease and arrhythmia,
 CC disorders associated with neovascularization and angiogenesis, for
 CC treating hypertrophic scars and keloids, ocular disorders e.g. diabetic
 CC retinopathy and uveitis, for wound healing and disorders of epithelial
 CC cell proliferation. The antibody is also useful for treating neurological
 CC diseases e.g. Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea and amyotrophic lateral sclerosis (ALS), diseases associated with
 CC increased apoptosis e.g. AIDS, toxin induced liver disease, septic shock,
 CC cachexia and anorexia, for preventing and healing damage to lungs and for
 CC treating infectious diseases. The present sequence represents the amino
 CC acid sequence of a novel human secreted protein. Note: the sequence data
 CC for this patent did not form part of the printed specification but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030065151
 CC
 XX Sequence 415 AA;
 SQ
 Query Match 100.0%; Score 2130; DB 6; Length 415;
 Best Local Similarity 100.0%; Pred. No. 4,4e-181;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 KCLAFYNGRNIFPLSPISISTAFSMLCLAQDSTLDEIKQGFNFRKMPKEXDLHEGFYII 120
 DB 61 KCLAFYNGRNITLSPISISTAFSMLCLAQDSTLDEIKQGFNFRKMPKEXDLHEGFYII 120
 QY 121 HELTQKTDKLSIGNTLFLDQRLQPRKEFLDPAKNFYSAETILTNFONLEMAQKQINDF 180
 DB 121 HELTQKTDKLSIGNTLFLDQRLQPRKEFLDPAKNFYSAETILTNFONLEMAQKQINDF 180
 QY 181 ISQKTHGKINNNILENDIPGVMLLNAVYIPFRANKHEPDPNTKEDDFLEKSSVYVPM 240
 DB 181 ISQKTHGKINNNILENDIPGVMLLNAVYIPFRANKHEPDPNTKEDDFLEKSSVYVPM 240
 QY 241 MFRSGIYGVYDDPKLSCTILIEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRWMTLLS 300
 DB 241 MFRSGIYGVYDDPKLSCTILIEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRWMTLLS 300
 QY 301 RRVADVSVPLNMTGTFPDLKKTLSYIGVSKIFREHGDLTAKIAPHSRLKVGAVHKAELKM 360
 DB 301 RRVADVSVPLNMTGTFPDLKKTLSYIGVSKIFREHGDLTAKIAPHSRLKVGAVHKAELKM 360
 QY 361 DERGTGAGTGAQTLPMETPLVYKTDKPYLLIYSEKIPSVLFLGKINVPYIGK 414
 DB 361 DERGTGAGTGAQTLPMETPLVYKTDKPYLLIYSEKIPSVLFLGKINVPYIGK 414

RESULT 8
 AAM78898
 ID AAM78898 standard; protein; 414 AA.
 XX
 AC AAM78898;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1560.
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001MO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-UTL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR MPI; 2001-476283/51.
 DR N-PSDB; AAK52031.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 PS
 PS Claim 20; Page 3878-3879; 6221bp; English.
 PS
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the

CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK5581), 2111
 CC (AAK5582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 CC
 XX Sequence 414 AA;
 XX

Query Match 99.7%; Score 2123; DB 4; Length 414;
 Best Local Similarity 99.8%; Pred. No. 1.8e-180;
 Matches 413; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTLGIAIFLAVALLVKGLIKSPSPRYKALSEVOGMQRMAAKELARONMDLGFKLL 60
 DB 1 MNPTLGIAIFLAVALLVKGLIKSPSPRYKALSEVOGMQRMAAKELARONMDLGFKLL 60
 QY 61 KKLAFYNGRNIFLSPISITAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHEGFYII 120
 DB 61 KKLAFYNGRNIFLSPISITAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHEGFYII 120
 QY 121 HEITQKTDKLSIGNTLFDORLQOPRKLEDAKNYSAETITNFQNLMAQKQINDF 180
 DB 121 HEITQKTDKLSIGNTLFDORLQOPRKLEDAKNYSAETITNFQNLMAQKQINDF 180
 QY 181 ISQTKGKINLLENIDPGVTMLLANYIFPRARKHEFDNVYKEEDPFLKSNSSVAVPM 240
 DB 181 ISQTKGKINLLENIDPGVTMLLANYIFPRARKHEFDNVYKEEDPFLKSNSSVAVPM 240
 QY 241 MFRSGIYQVGYDDKLSCTILIEIPYQXNITAFILPDEGKLEKLGQVDTFSWKTLIS 300
 DB 241 MFRSGIYQVGYDDKLSCTILIEIPYQXNITAFILPDEGKLEKLGQVDTFSWKTLIS 300
 QY 301 RRVVDVSVPLHMTGTPDKKTLSTYGVSKLFFEBHGLTCLIAHRSKAGBAVHAKELM 360
 DB 301 RRVVDVSVPLHMTGTPDKKTLSTYGVSKLFFEBHGLTCLIAHRSKAGBAVHAKELM 360
 QY 361 DERGTGAAGTGAQTLPMTETPLVVKIDKPYLLIYSEKISVFLGKIVPIGK 414
 DB 361 DERGTGAAGTGAQTLPMTETPLVVKIDKPYLLIYSEKISVFLGKIVPIGK 414

RESULT 9
 ABB11832
 ID ABB11832 standard; peptide; 431 AA.
 XX
 AC ABB11832;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human secreted protein homologue, SEQ ID NO:2202.
 XX
 XX

KM Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KM haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KM inhibin; chemokinesis; chemokinesis; thrombolysis; oncogenesis;
 KM proliferation; metastasis; cancer; tumor; haematopoietic disorder;
 KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KM chronic inflammatory condition; proliferative retinopathy;
 KM atherosclerosis; coronary heart disease; arterial ischaemia;
 KM bone disorder; osteoporosis; vascular growth disorder;
 KM tissue regeneration; wound healing; infection; immune disorder;
 KM cell culture; drug screening; gene therapy; anti-inflammatory;
 KM cytostatic; antiarthritis; haemostatic; antiarteriosclerotic;
 KM antifungal; vasoprotic; cardiant; virucide; antibacterial;
 KM
 XX
 XX Homo sapiens.

XX
 XX W0200157188-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 05-FEB-2001; 2001WO-US003800.
 XX
 XX 03-FEB-2000; 2000US-00496914.
 XX 27-APR-2000; 2000US-00560875.
 XX
 XX (HYSR-) HYSRQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 XX
 XX WPI: 2001-457740/49.
 XX DR N-PSDB; ABA09076.
 XX
 XX Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 XX Claim 20; Page 263; 1963pp; English.

XX
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX
 XX

Query Match 99.2%; Score 2114; DB 4; Length 431;
 Best Local Similarity 99.3%; Pred. No. 1.2e-179;
 Matches 411; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNPTLGIAIFLAVALLVKGLIKSPSPRYKALSEVOGMQRMAAKELARONMDLGFKLL 60
 DB 1 MNPTLGIAIFLAVALLVKGLIKSPSPRYKALSEVOGMQRMAAKELARONMDLGFKLL 77
 QY 61 KKLAFYNGRNIFLSPISITAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHEGFYII 120

```

Db      78 KKLAFYNGRNIFLSPISISTAFSMCLGAODSTLDEIKOGFNRFRMPKPKDLHEGFHYII 137
Qy      121 HELTQKTODLKLSIGNTLFIIDQRLQPKRKELEDAKNFYSAETILTNFQNLMAQKQINDF 180
Db      138 HELTQKTODLKLSIGNTLFIIDQRLQPKRKELEDAKNFYSAETILTNFQNLMAQKQINDF 197
Qy      181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRARWKHEPDNPVTKEDDFLEKNSSVKVPM 240
Db      198 IESKTHGKINNLIENIDPGTVMLLANYIFPRARWKHEPDNPVTKEDDFLEKNSSVKVPM 257
Qy      241 MFRSGIYQVGYDCKLSTCTILIEIPQKNITAFILPDGKLGKHLKGLQVDFSRMKTLLS 300
Db      258 MFRSGIYQVGYDCKLSTCTILIEIPQKNITAFILPDGKLGKHLKGLQVDFSRMKTLLS 317
Qy      301 RRVVDVSVPLHMTGTFDLKKTLSYIGSVKIFEEHGDLTFKIAPHRSLSKVGSAVHKAELKM 360
Db      318 RRVVDVSVPLHMTGTFDLKKTLSYIGSVKIFEEHGDLTFKIAPHRSLSKVGSAVHKAELKM 377
Qy      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
Db      378 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 431

```

RESULT 10

AA079882
ID AA079882 standard; protein; 431 AA.

AC AA079882;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3528.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KM nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

PN W0200157190-A2.

XX 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US004098.

XX 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00596075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-0064936.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

PA (HYSB-) HYSBQ INC.

PI Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

PI Ma Y, Zhao Qa, Wang D, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX WPI, 2001-476283/51.

DR N-PSDB; AAKS3015.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful

PT in diagnosis and gene therapy.

XX Claim 20; Page 371; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibit activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication

XX Sequence 431 AA;

Query Match 99.2%; Score 2114; DB 4; Length 431;

Best Local Similarity 99.3%; Pred. No. 1.2e-179;

Matches 411; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

Qy      1 MNPITGLAIFLAVLTVKGLKPSRPNRYKALSEVQKQMAAKELARQNDLGFKLL 60
Db      18 MNPITGLAIFLAVLTVKGLKPSRPNRYKALSEVQKQMAAKELARQNDLGFKLL 77
Qy      61 KKLAFYNGRNIFLSPISISTAFSMCLGAODSTLDEIKOGFNRFRMPKPKDLHEGFHYII 120
Db      78 KKLAFYNGRNIFLSPISISTAFSMCLGAODSTLDEIKOGFNRFRMPKPKDLHEGFHYII 137
Qy      121 HELTQKTODLKLSIGNTLFIIDQRLQPKRKELEDAKNFYSAETILTNFQNLMAQKQINDF 180
Db      138 HELTQKTODLKLSIGNTLFIIDQRLQPKRKELEDAKNFYSAETILTNFQNLMAQKQINDF 197
Qy      181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRARWKHEPDNPVTKEDDFLEKNSSVKVPM 240
Db      198 IESKTHGKINNLIENIDPGTVMLLANYIFPRARWKHEPDNPVTKEDDFLEKNSSVKVPM 257
Qy      241 MFRSGIYQVGYDCKLSTCTILIEIPQKNITAFILPDGKLGKHLKGLQVDFSRMKTLLS 300
Db      258 MFRSGIYQVGYDCKLSTCTILIEIPQKNITAFILPDGKLGKHLKGLQVDFSRMKTLLS 317
Qy      301 RRVVDVSVPLHMTGTFDLKKTLSYIGSVKIFEEHGDLTFKIAPHRSLSKVGSAVHKAELKM 360
Db      318 RRVVDVSVPLHMTGTFDLKKTLSYIGSVKIFEEHGDLTFKIAPHRSLSKVGSAVHKAELKM 377
Qy      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
Db      378 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 431

```

RESULT 11

AA005759
ID AA005759 standard; protein; 358 AA.

XX AA005759;

XX 24-OCT-2001 (first entry)

DE Human NOV7 polypeptide #2.

XX Human; NOV7; A132990 B; fertility disorder; spermatogenesis; cardiant;

KM cytostatic; immunomodulatory; antiproliferative; antidiabetic;

KM cell proliferation; cancer; diabetic retinopathy; angiodiabetic disorder;

KM pulmonary disorder; haematopoietic disorder; immunological disorder;

KM inflammatory disorder; tumour related disorders; emphysema; cirrhosis;

XX wound healing; gene therapy.

XX Homo sapiens.

XX Key location/Qualifiers

FT Misc-difference 311..322

FT /label= OTHER

XX /note= "Other= Unknown"

XX W0200149729-A2.

XX 12-JUL-2001.

```

PR 05-JAN-2001; 2001WO-US000239.
XX
XX 06-JAN-2000; 2000US-0174724P.
PR 11-JAN-2000; 2000US-0175434P.
PR 11-JAN-2000; 2000US-0175488P.
PR 12-JAN-2000; 2000US-0175696P.
PR 12-JAN-2000; 2000US-0175743P.
PR 13-JAN-2000; 2000US-0175819P.
PR 07-AUG-2000; 2000US-0223524P.
PR 04-JAN-2001; 2001US-00755665.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Prayaga SK, Majumder K, Tallon BE, Spaderna SK, Spytek KA,
PI Macdougall J,
XX
XX WPI; 2001-418356/44.
XX
XX Nucleic acid encoding polypeptides, designated NOVX polypeptides, useful
PT for treating a syndrome associated with a NOVX-associated disorder, e.g.
PT cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
PT pulmonary disorder.
XX
XX PS Disclosure; Page 33, 144pp; English.
XX
XX The invention relates to nucleic acids encoding NOVX (X being an integer
XX from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
XX useful in diagnosing, treating or manufacturing a medicament for a
XX disease or disorder associated with NOVX e.g. cell proliferation (cancer
XX and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
XX disorders (e.g. of spermatogenesis), haematopoietic, immunological,
XX inflammatory and tumour related disorders, emphysema, cirrhosis, wound
XX healing. NOVX nucleic acids are also useful in gene therapy. They are
XX also used for screening for a modulator of activity or of latency or
XX predisposition to a NOVX-associated disorder. They are also useful for
XX determining the presence of or predisposition to a NOVX-associated
XX disorder. The present sequence represents a version of NOV7 (A113290 B)
XX appearing in table 25 of the specification, which has sequence homology
XX to an unidentified human secreted protein (HMGUS54) and to alpha anti-
XX trypsin
XX
XX Sequence 358 AA;
SQ
Query Match 83.7%; Score 1783; DB 4; Length 358;
Best Local Similarity 96.6%; Pred. No. 3.3e-150;
Matches 346; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 54 DLGFKLLKLAFTNPGNIFLSPISISTASBMLCLGAQDSTLDEIRKQGFNRKMPKEDLH 113
DB 1 DLGFKLLKLAFTNPGNIFLSPISISTASBMLCLGAQDSTLDEIRKQGFNRKMPKEDLH 60
QY 114 EGFHYIIHELTKQTDKLSIGNTLFTDRLQPRKLEDAKNYSATLITNQNLEMA 173
DB 61 EGFHYIIHELTKQTDKLSIGNTLFTDRLQPRKLEDAKNYSATLITNQNLEMA 120
QY 174 OKQINDFISQKTHGKINNLLENIDPGTVMLANIIFPRARKHFEEDNVTKEEDFLEKN 233
DB 121 OKQINDFISQKTHGKINNLLENIDPGTVMLANIIFPRARKHFEEDNVTKEEDFLEKN 180
QY 234 SSYKVPMMFRSGIYQVGYDNLKSTLIEIFYQKNITAFILPDEGKLKHLKGLQVDTFS 293
DB 181 SSYKVPMMFRSGIYQVGYDNLKSTLIEIFYQKNITAFILPDEGKLKHLKGLQVDTFS 240
QY 294 RMTTLLSRVVDSVPLHMTGTPDLKKTSTYIGSVSKIFPEHGDULTKIAHRSIKVGEAV 353
DB 241 RMTTLLSRVVDSVPLHMTGTPDLKKTSTYIGSVSKIFPEHGDULTKIAHRSIKVGEAV 300
QY 354 HKAEKMDERGTGAAGTGAQTLEMETPLVVKIDKPYLLIYSKIPSVLFLGKIYVP 411
DB 301 HKAEKMDERGTGAAGTGAQTLEMETPLVVKIDKPYLLIYSKIPSVLFLGKIYVP 358
RESULT 12

```

```

AAP50877
ID AAP50877 standard; protein; 418 AA.
XX
XX AAP50877;
AC AAP50877;
XX
XX 25-MAR-2003 (revised)
DT 16-AUG-2002 (revised)
DT 03-SEP-1991 (first entry)
XX
XX Sequence encoded by human alpha-1-antitrypsin (alpha-1-AT) cDNA.
XX
XX Leukocyte elastase inhibitor; emphysema therapy; lung disease.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 125
FT /note= "Arg in published SQ"
FT Misc-difference 139
FT /note= "Asp in published SQ"
FT Misc-difference 140
FT /note= "Gly in published SQ"
FT Misc-difference 237
FT /note= "Ala in published SQ"
FT Misc-difference 273
FT /note= "Asn in published SQ"
FT Misc-difference 326
FT /note= "Val in published SQ"
FT Region 382..383
FT /label= Reactive centre
XX
XX EP164719-A.
XX
XX 18-DEC-1985.
XX
XX 14-JUN-1984; 84US-00620408.
XX
XX 14-JUN-1984; 84US-00620408.
XX
XX 14-JUN-1984; 84US-00620408.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Barr PJ, Halliwell RA, Rosenberg S, Brake AJ;
PI WPI; 1985-318257/51.
XX
XX N-PSDB; AAN50540.
XX
XX Polypeptide oxidative stable serine protease inhibitor - having human
PT alpha-1-antitrypsin amino-acid sequence with neutral amino-acid at active
PT site.
XX
XX Example; Page 16; 37pp; English.
XX
XX The inventors claim a polypeptide oxidative stable human leukocyte
CC elastase inhibitor differing from wild type human alpha-1-AT by fewer
CC than 10 AAs and having the methionine at the active site (see AAP50877)
CC substituted with a neutral oxidatively stable AA, pref. Val or Ala.
CC (Updated on 16-AUG-2002 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PA field.)
XX
XX Sequence 418 AA;
SQ
Query Match 37.3%; Score 795; DB 1; Length 418;
Best Local Similarity 43.0%; Pred. No. 6.3e-62;
Matches 156; Conservative 74; Mismatches 131; Indels 2; Gaps 1;
QY 54 DLGFKLLKLAFTNPGNIFLSPISISTASBMLCLGAQDSTLDEIRKQGFNR--KMPKED 111
DB 56 EFAFSLYRDLAHHSNSTNIFSPVSATAPAMLSLTKADTHDEILGALFNLTETPEAQ 115
QY 112 LHEGFHYIIHELTKQTDKLSIGNTLFTDRLQPRKLEDAKNYSATLITNQNLE 171
DB 112 LHEGFHYIIHELTKQTDKLSIGNTLFTDRLQPRKLEDAKNYSATLITNQNLE 171

```


Oy		352	A V H K A E L I M D E R G T E G C A A G T G A Q T L P M E R P L V Y K I D K P L L I I Y S E K R I S V F I G K I N P	411
			: : : : : : : : : : : : : : : : : : : :	
Dd		356	A V H K A V L I I D E R G T E A A G A M F L E A I P M S I P P V K F K P E F V F L M I B O N T S P L F M G K V N P	415
Oy		412	I G K	414
Dd		416	T Q K	418

Search completed: March 31, 2006, 09:46:07
Job time : 192 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: March 31, 2006, 09:46:24 ; Search time 41 Seconds
(without alignments)
971.555 Million cell updates/sec

Title: US-10-664-356-1562
Sequence: 1 MNPTGLIAFLAVLLTVKGL.....YSEKIPSVLFGKIVNPGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	787	36.9	409	1	ITBA
2	785.5	36.9	413	1	SS4981
3	785	36.9	411	1	ITRT
4	785	36.9	418	1	ITRU
5	782	36.7	406	2	JX0346
6	780.5	36.6	413	2	JX0154
7	778.5	36.5	413	2	JX0267
8	775.5	36.4	413	2	AS4968
9	768.5	36.1	413	2	149470
10	766.5	36.0	413	2	149472
11	760.5	35.7	413	2	149452
12	758.5	35.6	413	2	149453
13	756	35.5	402	2	149471
14	753	35.4	413	2	S60036
15	747.5	35.1	408	2	S11320
16	745.5	35.0	416	2	B29131
17	743	34.9	403	2	S08102
18	742.5	34.9	413	2	149474
19	742	34.8	416	2	S21097
20	731	34.3	418	1	S31507
21	728.5	34.2	406	2	A39339
22	728	34.2	416	1	ITSH
23	726.5	34.1	418	2	JH0494
24	725.5	34.1	410	2	AA5457
25	717	33.7	405	2	A39088
26	716	33.6	383	2	A36117
27	714	33.5	413	2	156481
28	710.5	33.4	418	2	S23675
29	707	33.2	412	1	ITMSC

30	702	33.0	418	2	JX0129	contrapsin precurs
31	701	32.9	412	2	S31505	serine proteinase
32	701	32.9	417	2	S19724	kallikrein-binding
33	698.5	32.8	415	2	A47224	thyroxine-binding
34	696	32.7	430	2	A49190	corticosteroid-bin
35	686	32.2	412	2	146421	thyroxine-binding
36	685.5	32.2	418	2	A39567	thyroxine-binding
37	684.5	32.1	406	2	153281	corticosteroid-bin
38	680	31.9	410	2	C39088	contrapsin precurs
39	678.5	31.9	433	1	ITHUC	alpha-1-antichymot
40	674	31.6	405	2	A28321	corticosteroid-bin
41	663	31.1	410	2	150494	serine proteinase
42	651.5	30.6	388	2	B39088	alpha-1-antiprotei
43	644.5	30.3	436	2	A42440	estrogen-regulated
44	629	29.5	427	2	A49518	kallikrein precurs
45	620.5	29.1	369	2	JH0493	alpha-1-antichymot

ALIGNMENTS

RESULT 1

ITBA
alpha-1-antitrypsin precursor - baboon (fragment)
N/Alternate names: alpha-1-proteinase inhibitor
C/Species: Papio sp. (baboon)
C/Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 05-Oct-2004
C/Accession: A01248
R/Kurachi, K.; Chandra, T.; Degen, S.J.F.; White, T.T.; Marchioro, T.L.; Woo, S.L.C.; Day
Proc. Natl. Acad. Sci. U.S.A. 78, 6826-6830, 1981
A/Title: Cloning and sequence of cDNA coding for alpha-1-antitrypsin.
A/Reference number: A01248; MUID:82082539; PMID:7031661
A/Accession: A01248
A/Molecule type: mRNA
A/Residues: 1-409 <KUR>
C/Cross-references: UNIPARC:UPI0000124FDC; GB:U00321; NID:G176561; PIDN:AAA5377.1; PID:
C/Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary target
psin.
C/Superfamily: serpin
C/Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F/1-15/Domain: signal sequence (fragment) #status predicted <Sig>
F/16-409/Product: alpha-1-antitrypsin #status predicted <MAT>
F/61,98,262/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/373/Inhibitory site: Met (elastase, collagenase) #status predicted

Query Match	36.9%	Score 787	DB 1	Length 409
Best Local Similarity	41.9%	Pred. NO. 8e-47		
Matches 152	Conservative 82	Mismatches 127	Indels 2	Gaps 1
QY	54	DLPKLLKLAFAVNPGRNIFLSPSTARSMLCAGDSLTDEIKGFNFR--KMPKND 111		
DB	47	EPAPSLYRQLAHOSNSTIFSPSIVATAPAMSLGKADTBHILGMLFNLTETBEAQ 106		
QY	112	LHSGFYTHIELTQKQDLSIGNTLFIDRLOPOQKFLPDANKFSAETILTNPNLE 171		
DB	107	VHSGFQELAKTLKKPDSQLQITGNGFLANKSLKVVDFLEADYKNLYHSAPSNFEDYE 166		
QY	172	MAQKQINDFISQTHGKINNLINIDPGIVMLLANYIFPRAKWKHEFDNPVTKEDDFLE 231		
DB	167	EAKQKQINNVKETOGLQGVLDLVKELDRDVFALVANYIFFGKWKRPPEVATEBEDPHVD 226		
QY	232	KNSSVYPMMPFRSGITQVGVDDLSCTIILEIPQKNTAIFILPDEKLGHLKGLQVDT 291		
DB	227	QATTVKVPMMRRILGMFNIYHCEKLSMWLLMKVLGNATLFLPDEKQLHLENELTHDI 286		
QY	292	FSRKKTLISRRVDVSVPLAMTGFPLDKTSLYIGVSKIFEEHGDITKIAPRSLKVG 351		
DB	287	ITFPLENENRNSANLHLPKLATITGYDLKTVLGHGILTKFNSGADISGTEBAPLKSK 346		
QY	352	AVHKAELKQDERGTGGAAGTAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFGKIVNP 411		
DB	347	AVHKAVALTIDKGTGAAGMFLBALPMSIFPEVKFNKPFVFLMIQVTKSPPLFGKVVNP 406		

QY 412 IGR 414
DB 407 TQK 409

RESULT 2

S54981

alpha-1-antiprotease isoform B precursor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 05-Oct-2004

C/Accession: S54981, S72199

R/Salt: A.; Sinohara, H.

Biochem. J. 307, 369-375, 1995

A/Title: Rabbit alpha-1-antiprotease B: a novel recombinant serpin which does not inhibit

A/Reference number: S54981, MUID:95251597, PMID:7733871

A/Accession: S54981

A/Molecule type: mRNA

A/Residues: 1-413 <SA12>

A/Cross-references: UNIPROT:Q28665; UNIPARC:UPI0000086790; EMBL:D17725; NID:g1008927; PI

A/Accession: S72199

A/Molecule type: protein

A/Residues: 25-33;374-387 <SA12>

A/Cross-references: UNIPARC:UPI0000176311; UNIPARC:UPI0000176312

C/Superfamily: serpin

C/Keywords: acute phase; emphysema; glycoprotein; plasma; serine proteinase inhibitor

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-413/Product: alpha-1-antiprotease B #status experimental <MAT>

Query Match

Best Local Similarity 36.9%; Score 785.5; DB 2; Length 413;

Matches 155; Conservative 98; Mismatches 155; Indels 5; Gaps 2;

QY 1 NMPTGLAIFLAVLTWKGLKPSFPRNYKALSEVQGMKQMAKELARQNMDLGFKLL 60

DB 1 MPPSVRAL---LLAGLGCLPGLFLADENQETRAVSSHEDDHAQCHRIPSLALFALSLY 57

QY 61 KGLAFNPGRNIFLPSLISSTAFSMCLGAQDSTLDEIKQG--FNPRKPEKDLHEGFHY 118

DB 58 REVAHSNNTNIFPFSVSIATAPAMLSLAKGSDTHQVLEGLKFNLTETAEQIHDOFRH 117

QY 119 IHELTQKTDKLSIGNTLFTDRLQPKRFLKEDAKNFSATITLTNPNLEMAQKQIN 178

DB 118 LHTVNRPDSEQLQLAGNMLVHENIKLQHKFLKEDAKNQLQSEAFVDFDPQQAQTKIN 177

QY 179 DFLSQTHKINNLINIDPGVLMALNTYIFPRAKMHEFDPNVTKKEPFLKSSVYK 238

DB 178 SHVEKTRKGIYDVLVDELARTILALVNTYVFFKGMKEKPEPNTKEDPHVDATTYK 237

QY 239 PMWFSGIYQVGYDDKLSITLIEIPYQKNITAFILPDEGKLHLEKGLQVDTFSRWKTU 298

DB 238 PMWSRLGMYVFMFCSLTASTVLMYKGNATLFLPDEGKLQHLBDTLTTELIAKFLAK 297

QY 299 LSRVAVDVPRRLHMTGTDLKKTLSYIGVSKIFEEHGDITKJAPRSLKVGAVKAE 358

DB 298 SFLRSTVYFPPKLSISGTDLKPLKGLKGTQVFSNNADLSGTEDEPLKVSQALHKA 357

QY 359 KMDERTEGAAGAGTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIVNP 411

DB 358 TIDERTGAAGASFVLEIPESVDSITLDRPFLFVLIYSHKISPLVGVKIVNP 410

RESULT 3

ITRT

alpha-1-antitrypsin precursor - rat

N/Alternate names: alpha-1-proteinase inhibitor

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Mar-1992 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004

C/Accession: A33892; B33892; S08016; JX0123; A38823

R/Chao, S.; Chai, K.X.; Chao, L.; Chao, J.

Biochemistry 29, 323-329, 1990

A/Title: Molecular cloning and primary structure of rat alpha-1-antitrypsin.

A/Reference number: A33892; MUID:90148955; PMID:2302382

A/Accession: A33892

A/Molecule type: mRNA

A/Residues: 4-411 <CHA>

A/Cross-references: UNIPROT:P17475; UNIPARC:UPI0000170896; GB:M32247; NID:g203062; PIND:J

A/Accession: B33892

A/Molecule type: protein

A/Residues: 25-57 <CH2>

A/Cross-references: UNIPARC:UPI00001731P9

R/Fink, I.L.; Bailey, T.; Morlin, B.

submitted to the EMBL Data Library, August 1989

A/Reference number: S08016

A/Accession: S08016

A/Molecule type: mRNA

A/Residues: 188-246; 'I', 248-321, 'D', 323-389 <FL1>

A/Cross-references: UNIPARC:UPI0000170827; EMBL:X16273; NID:957299; PIND:CAA34349.1; PID:

R/Masumi, Y.; Sohma, M.; Ohkubo, K.; Takami, N.; Oda, K.; Ikehara, Y.

J. Biochem. 108, 230-234, 1990

A/Title: Molecular cloning and sequencing of the cDNA of rat alpha-1-protease inhibitor

A/Reference number: JX0123; MUID:91035351; PMID:2229024

A/Accession: JX0123

A/Molecule type: mRNA

A/Residues: 1-13; 'G', 15-83; 'V', 85-247; 'Y', 249-317; 'N', 319-411 <MIS>

A/Cross-references: UNIPARC:UPI000016797B; GB:D00675; NID:g220648; PIND:BA00579.1; PID:

A/Experimental source: serum

A/Accession: A38823

A/Molecule type: protein

A/Residues: 25-45 <MI2>

A/Cross-references: UNIPARC:UPI00001731PA

C/Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary target

psin.

C/Superfamily: serpin

C/Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-411/Product: alpha-1-antitrypsin #status experimental <MAT>

F/44,101,265/Binding site: carbohydrate (Asn) (covariant) #status predicted

F/76/Inhibitory site: Met (elastase, collagenase) #status predicted

Query Match

Best Local Similarity 36.9%; Score 785; DB 1; Length 411;

Matches 161; Conservative 94; Mismatches 150; Indels 10; Gaps 5;

QY 1 NMPTGLAIFLAVLTWKGLKPSFPRNYKALSEVQGMKQMAKELARQNMDLGFKLL 60

DB 1 MAPSISRGILLALALC---CLAPSFLEADAQETDTSQDQSPVYRKISSNLADPAFSLY 56

QY 61 KGLAFNPGRNIFLPSLISSTAFSMCLGAQDSTLDEIKQG--FNPRKPEKDLHEGFHY 118

DB 57 RELVHOSNTSNIFPFSMTITTPAMLSLSSKQDTRKQILEGELNLTQLEADDIKAFH 116

QY 119 IHELTQKTDKLSIGNTLFTDRLQPKRFLKEDAKNFSATITLTNPNLEMAQKQIN 178

DB 117 LQTLNRPDSEQLQNTGNGLFVNKQIKLVEKFLKEVKNYHSEARSVNADSEAKVIN 176

QY 179 DFLSQTHKINNLINIDPGVLMALNTYIFPRAKMHEFDPNVTKKEPFLKSSVYK 238

DB 177 DVEKGTQKIDVLMKQLEDIVFALVNTYIFPKGMKKEPFEHHRDADFVHDKSTTVY 236

QY 239 PMWFSGIYQVGYDDKLSITLIEIPYQKNITAFILPDEGKLHLEKGLQVDTFSRWKTU 298

DB 237 PMWRLGMDMYCTSLSSWVLMYLGNAATLFLPDEGKLQHLBDTLTTELIAKFLAK 294

QY 299 LSRVAVDVPRRLHMTGTDLKKTLSYIGVSKIFEEHGDITKJAPRSLKVGAVKAE 356

DB 295 LNRQTRSAIYPPKLSISGTYNLKTLSLGIITRVFNNDADLSGITEDAPLKSQAVHKA 354

QY 357 ELKMDERTEGAAGAGTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIVNP 411

DB 355 VLTLDERTGAAGATVVEAVPWSLPQVYFDPFIFMVESETQSPPLFVGKIVNP 409

RESULT 4

ITRU

alpha-1-antitrypsin precursor [validated] - human

N/Alternate names: alpha-1-AI; alpha-1-proteinase inhibitor

C;Species: Homo sapiens (man)
C;Date: 30-Nov-1980 #sequence revision 31-Mar-1992 #text change 05-Oct-2004
C;Accession: A21853; B21853; A93352; A90944; A58528; A23174; A93281; A23336; S14476; A24
B10ng, G.L.; Chandra, T.; Woo, S.L.C.; Davie, E.W.; Kurachi, K.
A;Title: Complete sequence of the cDNA for human alpha-1-antitrypsin and the gene for th
A;Reference number: A21853; MUID:85047190; PMID:6093867
A;Accession: A21853
A;Molecule type: mRNA
A;Residues: 1-418 <LON1>
A;Cross-references: UNIPROT:P01009; UNIPARC:UP1000000CBEBC; GB:K02212; NID:9177830
A;Experimental source: M (normal) allele
A;Accession: B21853
A;Molecule type: DNA
A;Residues: 1-287, 'V', 289-418 <LON2>
A;Cross-references: UNIPARC:UP1000016A3A8; GB:K02212; NID:9177830; PIDN:AA59495.1; PID:
A;Experimental source: S variant allele
R;Roederberg, S.; Barr, P.J.; Najarian, R.C.; Halliwell, R.A.
A;Title: Synthesis in yeast of a functional oxidation-resistant mutant of human alpha-1-
A;Reference number: A93352; MUID:85036645; PMID:6387509
A;Accession: A93352
A;Molecule type: mRNA
A;Residues: 1-124, 'H', 126-325, 'I', 327-418 <ROS>
A;Cross-references: UNIPARC:UP1000014IDE5; EMBL:X01683; NID:928965
R;Bollen, A.; Herzog, A.; Cravador, A.; Herion, P.; Chuchana, P.; Vander Straten, A.; Lo
DNA 2, 255-264, 1983
A;Title: Cloning and expression in Escherichia coli of full-length complementary DNA cod
A;Reference number: A90944; MUID:84107980; PMID:6319097
A;Accession: A90944
A;Molecule type: mRNA
A;Residues: 1-138, 'DR', 141-272, 'N', 274-418 <BOL>
A;Cross-references: UNIPARC:UP10001731BF; GB:K01396; NID:928965
A;Note: this sequence has been corrected in reference A58528
R;Colau, B.; Chuchana, P.; Bollen, A.
DNA 3, 327-330, 1984
A;Title: Revised sequence of full-length complementary DNA coding for human alpha-1-ant
A;Reference number: A58528; MUID:85026667; PMID:6333329
A;Contents: corrections to sequence in A90944
A;Accession: A58528
A;Molecule type: mRNA
A;Residues: 1-418 <COL>
A;Cross-references: UNIPARC:UP100000CBEBC; GB:K01396; NID:928965; PIDN:CAA5838.1; PID:G
R;Ciliberto, G.; Dente, L.; Cortese, R.
Cell 41, 531-540, 1985
A;Title: Cell-specific expression of a transfected human alpha-1-antitrypsin gene.
A;Reference number: A23174; MUID:85176977; PMID:2985281
A;Accession: A23174
A;Molecule type: mRNA
A;Residues: 1-11, 13-173, 'H', 175-228, 'D', 230-418 <CIL>
A;Cross-references: UNIPARC:UP100016A3A7; GB:M11465; NID:9177826; PIDN:AA51546.1; PID:
A;Note: the authors state that this sequence corresponds to the M (normal) allele; 3 var
R;Carrell, R.W.; Jeppsson, J.O.; Laurell, C.B.; Brennan, S.O.; Owen, M.C.; Vaughan, L.;
Nature 298, 339-344, 1982
A;Title: Structure and variation of human alpha-1-antitrypsin.
A;Reference number: A93281; MUID:82220135; PMID:7045697
A;Accession: A93281
A;Molecule type: Protein
A;Residues: 25-418 <CAR>
A;Cross-references: UNIPARC:UP1000014E11
A;Note: peptide sequence differences with A21853 (Leu-200 and the amidation states of re
R;Zhu, X.Y.; Kang, S.S.; Hargrove, K.; Shochat, D.; Jarrells, M.; Moesley, M.; Chan, S.K
Biochem. J. 246, 25-36, 1987
A;Title: The identification of epitopic sites in human alpha-1-proteinase inhibitor.
A;Reference number: A32336; MUID:86049621; PMID:2445337
A;Accession: A32336
A;Molecule type: Protein
A;Residues: 25-418 <ZHU>
A;Cross-references: UNIPARC:UP1000014E11
A;Note: peptides were sequenced or partially sequenced and ordered by comparison with A2
R;Welland, K.L.; Palany, C.N.; Dooley, T.P.
Submitted to the EMBL Data Library, December 1989
A;Description: Identification of a cDNA encoding a variant form of the human proteolytic

A;Reference number: S14476
A;Accession: S14476
A;Molecule type: mRNA
A;Residues: 142-230, 'Y', 232-338 <WEI>
A;Cross-references: UNIPARC:UP1000006E0F9; EMBL:X17122; NID:928636; PIDN:CAA34982.1; PID
A;Experimental source: a variant form
R;Riley, J.H.; Bachurst, I.C.; Edcrooke, M.R.; Carrell, R.W.; Craig, R.K.
FEBS Lett. 189, 361-366, 1985
A;Title: Alpha-1-antitrypsin and serum albumin mRNA accumulation in normal, acute phase
A;Reference number: A24013; MUID:86003469; PMID:3876243
A;Accession: A24013
A;Molecule type: mRNA
A;Residues: 292-418 <RIL>
A;Cross-references: UNIPARC:UP1000016A3A9; EMBL:X02920; NID:924437; PIDN:CAA26677.1; PID
R;Schulze, A.J.; Baumann, U.; Krof, S.; Jaeger, E.; Huber, R.; Laurell, C.B.
Eur. J. Biochem. 194, 51-56, 1990
A;Title: Structural transition of alpha(1)-antitrypsin by a peptide sequentially similar
A;Reference number: S13833; MUID:91071209; PMID:2253623
A;Accession: S13833
A;Molecule type: Protein
A;Residues: 25-41 <SCH>
A;Cross-references: UNIPARC:UP100001731F0
R;Niemann, M.A.; Narkates, A.J.; Miller, E.J.
Matrix 12, 233-241, 1992
A;Title: Isolation and serine protease inhibitory activity of the 44-residue, C-terminal
A;Reference number: S23516; MUID:93024095; PMID:1406456
A;Accession: S23516
A;Molecule type: Protein
A;Residues: 375-409, 'L', 411-413, 'S' <NIE>
A;Cross-references: UNIPARC:UP10000070F7B
R;Dengler, R.; Eger, G.; Lotzpeich, F.; Plewan, A.; Ogilvie, A.; Emmerich, B.
Biol. Chem. Hoppe-Seyler 376, 165-172, 1995
A;Title: Limited proteolysis of alpha(1)-proteinase inhibitor (alpha(1)-PI) in acute leu
A;Reference number: S55249; MUID:95336645; PMID:7612193
A;Accession: S55249
A;Molecule type: Protein
A;Residues: 25-28, 43-47, 207-208, 382-389, 414-418 <DS2>
A;Cross-references: UNIPARC:UP100001583FA; UNIPARC:UP100001731F3; UNIPARC:UP100001731F4;
R;Leicht, M.; Long, G.L.; Chandra, T.; Kurachi, K.; Kidd, V.J.; Mace, M.
Nature 297, 655-659, 1982
A;Title: Sequence homology and structural comparison between the chromosomal human alpha
A;Reference number: I39371; MUID:82220035; PMID:6979715
A;Accession: I39371
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 196-225 <LEI2>
A;Cross-references: UNIPARC:UP1000016A3A6; GB:J00066; NID:9177819; PIDN:AA59370.1; PID:
R;Chang, W.S.W.; Wardell, M.R.; Lomas, D.A.; Carrell, R.W.
Biochem. J. 314, 647-653, 1996
A;Title: Probing serpin reactive-loop conformations by proteolytic cleavage.
A;Reference number: S63599; MUID:96239126; PMID:8670081
A;Accession: S63599
A;Molecule type: Protein
A;Residues: 371-385 <CHA>
A;Cross-references: UNIPARC:UP100001731F7
R;Coutelle, C.; Speer, A.; Rogers, J.; Kalsheker, N.; Humphries, S.; Williamson, R.
Biomed. Biochem. Acta 44, 421-431, 1985
A;Title: Construction and partial characterization of a human liver cDNA library.
A;Reference number: I39370; MUID:85225507; PMID:3873938
A;Accession: I39370

A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 387-399, 'D', 401-418 <CUG>
A/Cross-references: UNIPARC:UPI0000163AA; GB:M26123; NID:gl77815; PIDN:AA51545.1; PID:
R/Faber, J.P.; Weidinger, S.; Olek, K.
Am. J. Hum. Genet. 46, 1158-1162, 1990
A/Title: Sequence data of the rare deficient alpha-1-antitrypsin variant PI Zausberg.
A/Reference number: A35338; MUID:90252805; PMID:2339709
A/Accession: A35338
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 122-124, 'H', 126-128, 363-365, 'K', 367-369 <FAB>
A/Cross-references: UNIPARC:UPI000147271; UNIPARC:UPI00001731F8
A/Experimental source: mutant PI Zausberg
A/Note: this 2 mutation with Lys-366 arose from the M2 variant with His-125
R/Joebmann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A/Reference number: A50775; PDB:7AP1
A/Contents: annotation; X-ray crystallography, 3.0 angstroms, tetragonal form 1, residue
R/Joebmann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A/Reference number: A50794; PDB:8AP1
A/Contents: annotation; X-ray crystallography, 3.1 angstroms, hexagonal form, residues 4
R/Joebmann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A/Reference number: A50810; PDB:9AP1
A/Contents: annotation; X-ray crystallography, 3.0 angstroms, tetragonal form 2, residue
J. Mol. Biol. 177, 531-556, 1984
A/Title: Human alpha-1-proteinase inhibitor. Crystal structure analysis of two crystal
A/Reference number: A58525; MUID:84292309; PMID:6332197
A/Contents: annotation; X-ray crystallography, 3.0 angstroms
R/Carelli, R.W.; Jeppesen, J.O.; Vaughan, L.; Brennan, S.O.; Owen, M.C.; Boswell, D.R.
FEBS Lett. 135, 301-303, 1981
A/Title: Human alpha-1-antitrypsin: carbohydrate attachment and sequence homology.
A/Reference number: A58526; MUID:82056611; PMID:6976274
A/Contents: annotation; carbohydrate attachment sites
A/Comment: The Z variant allele has Lys-366. Deficiency of the normal inhibitor in indiv
sib.
C/Genetic:
A:Gene: GDB:PI
A:Cross-references: GDB:120289; OMIM:107400
A:Map position: 14q32.1-14q32.1
A:Introns: 216/1; 306/2; 355/3
A/Note: the first intron occurs before the initiator codon
C/Function:
A:Description: inhibitor of serine proteinases, primarily leukocyte elastase and collagen
A/Note: It also inhibits plasmin, chymotrypsin, kallikrein, trypsin, and chymotrypsin
C/Superfamily: serpin
C/Keywords: acute phase; emphysema; glycoprotein; plasma; polymorphism; serine proteinase
F/1-24/Domain: signal sequence #status predicted <SIG>
F/25-418/Product: alpha-1-antitrypsin #status experimental <MAT>
F/70,107,271/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 36.7%; Score 785; DB 1; Length 418;
Best Local Similarity 42.7%; Pred. No. 1.7e-46;
Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;
Db 54 DLGPKLLKLAAPRNPTFLSLSTASTASMLCLGAQDSTLDEIKQFNR--KRPKD 111
Db 56 EFAFSYLRQALHOSNSTNIFSPVSATATAPAMSLGKADTHDEILGLENFNLTEIPBAQ 115
Qy 112 LHEGFYIITHELQTKODLKGISGNTLFDIQLQPKFLEDAKNFSAETILTNQONLE 171
Db 116 IHGFPQLRLTNQPSQQLQTLTGNGFLFSEGLKVDKFLBDYKGLYHSAFVYNGDTE 175
Qy 172 MAQKQINDPISQKTHGKINNLEINIDPGYVLLMANTYIFPARMKHEPDPVNTKEEDPFL 231
Db 176 EAKKQINDYVEKGTQKQIVDLVKELRDVTFAVLNNTYIFFGKWERPFEVDTEEDFHYD 235
Qy 232 KNSSVVPMFRRSGIYOVGDGKLSCTILEIPYQKNITAFILPDGKGLKHLKGLQVPT 291
Db 236 QVTVAVPMKRLGMFNIOHCKRLSSVLLMKYLGNAATLFLPDGKQLHLENLTHDI 295

Qy 292 FSRKTLISRRVVDVSPRLMTGTFDLKKTLSYGVSKEEFGDLTKIAPRSKVG 351
Db 296 ITTFLENEBRKASLHLPKLSTIGTDYKGLQGLITKFSGALLSGTEBAPLKSK 355
Qy 352 AVHKAELKDERGTGGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFGKIVP 411
Db 356 AVHKAVALTEDEKTEAAGAFLEAIPLMSIPPEVKFNKPFVFLMI EQNTKSPLFMGKVP 415
Qy 412 IGR 414
Db 416 TQK 418
RESULT 5
JX0346
C/Species: Meriones unguiculatus (Mongolian jird)
C/Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 05-Oct-2004
C/Accession: JX0346; PC2357
R/Goto, K.; Suzuki, Y.; Yoshida, K.; Yamamoto, K.; Shinohara, H.
J. Biochem. 116, 582-588, 1994
A/Title: Plasma alpha-1-antiproteinase from the Mongolian gerbil, Meriones unguiculatus.
A/Reference number: JX0346; MUID:95155268; PMID:7852275
A/Accession: JX0346
A/Molecule type: mRNA
A/Residues: 1-406 <GOT>
A/Cross-references: UNIPROT:Q64118; UNIPARC:UPI000008496; GB:S77822; NID:g998663; PIDN:/
A/Accession: PC2357
A/Molecule type: protein
A/Residues: 25-44, 77-96 <GQ2>
A/Cross-references: UNIPARC:UPI000017630E; UNIPARC:UPI000017630F
A/Experimental source: plasma
C/Superfamily: serpin
C/Keywords: glycoprotein
F/1-24/Domain: signal sequence #status predicted <SIG>
F/25-406/Product: alpha-1-antiproteinase #status predicted <MAT>
F/383-387/Region: serpin binding #status predicted
F/59,96,134,260,403/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/371/Inhibitory site: Met (trypsin, chymotrypsin, elastase) #status predicted
Query Match 36.7%; Score 782; DB 2; Length 406;
Best Local Similarity 41.3%; Pred. No. 1.7e-46;
Matches 166; Conservative 84; Mismatches 142; Indels 10; Gaps 4;
Db 14 LTLVKGTL--IKSPFSRNRKALSEVQGWKQMAAKSLAQNMDLGGKLLKLAFAVPRN 71
Db 9 LTLMAQLCCLVPSFLAED--AEKTDSSHODHMASMLA---DPAFLYRVLSHOSNTTN 62
Qy 72 IFPLSLSTASTASMLCLGAQDSTLDEIKQF--FNPRKMPKDLHEGFYIITHELQTKOD 129
Db 63 IFPLSPSTNTALAMSLSGSKDPTKQQLQGLHFNLTSEADHINKFQHLTKTLNPNB 122
Qy 130 LKISGNTLFDIQLQPKFLEDAKNFSAETILTNQONLEMAQKQINDPISQKTHGKI 189
Db 123 LQTLTSSSLFVNNSLNLVLEKFLSEVGNHNSFAFVNFADSEBAKKTINSFVEKATHGKI 182
Qy 190 NNLINIDPGTYMLANTYIFPARMKHEPDPVNTKEEDFLEKNSVVKVPMFRRSGIYOV 249
Db 183 VDLVQLELDITVALNNTYIFFGKWERPFEVDTEADHVDSTVVKVPMFRRKMGFV 242
Qy 250 GYDDKLSCTILIPYQKNITAFILPDEKGLKHLKGLQVDPFSRKTLISRRVVDVSP 309
Db 243 HXCDSLSSVLLMDYGNATAFILPDEKGMHLBQTLKHNHYKRLQNRHRSANVHP 302
Qy 310 RLHMTGTFDLKKTLSYGVSKEEFGDLTKIAPRSKLVGAHVHKAELKMDERGTGGA 369
Db 303 KLSISGTYMLKKVLSPLGITGVFVNSGADISGTTVDPLKLSRAVHKAVALTLDERGTGAAG 362
Qy 370 GTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFGKIVP 411
Db 363 TVLEAVPMSPDPVCFKRPVVLICDKATQSPFLFVGKVP 404

RESULT 6
 JX0154
 alpha-1-antiprotease F - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 05-Oct-2004
 C/Accession: JX0154
 R/Saito, A.; Sinohara, H.
 J. Biochem. 109, 158-162, 1991
 A/Title: Cloning and sequencing of cDNA coding for rabbit alpha-1-antiprotease F: amir
 A/Reference number: JX0154; MUID:91201273; PMID:2016265
 A/Accession: JX0154
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-413 <SAI>
 A/Cross-references: UNIPROT:P23035; UNIPARC:UPI0000024FCB; GB:X57710; NID:g1455; PIDN:CA
 C/Superfamily: serpin

Query Match 36.6%; Score 780.5; DB 2; Length 413;
 Best Local Similarity 37.5%; Pred. No. 2.3e-46;
 Matches 155; Conservative 96; Mismatches 157; Indels 5; Gaps 2;

QY 1 MNPTLGAIPLAVLLTVKGLKPSFSPRYKALSEVQGMKQMAAKELARQNMDLGFKLL 60
 Db 1 MPFSVSRAL---LLLAGIGCLLPGLADEAQETAVSSHEDHPACHRIAPSLAEFALSLY 57
 QY 61 KKLAFYNGRNIFLSPISITAFSMLCLGAQDSTLDEIKQG--FNFRKMPKDLHEGFHY 118
 Db 58 REVAHESNTNTNIFSPVISALAFAMLSLGAAGDTHTVLEGLKFNLTETAAQIHDFGRH 117
 QY 119 IIEHLQKTDKLSIGNTLFIIDRLQPORKEFLDANKFSAETILTNFONLEMAQKQIN 178
 Db 118 LHTVNRPDSELOLAAGNALVHENTLQHKFLEDAKQLQSEAFVDFPDPEQAKTKIN 177
 QY 179 DFIQKTHGKINLNIENIDPGTWMLANYIFPRARKHEDPNVTKEDDFLEKNSSVKY 238
 Db 178 SHVEKGTGRKIVDLVQELDARTLLALVNVYFFKGMKEKPEPENTKEDDFVDAATTVRV 237
 QY 239 PMFRSGIYGVYDDKLSCTILFIYQKNTAIFILPDEGQLKLEKGLQVDTFSRKTL 298
 Db 238 PMMSRLGRYDLFHCSTLASVTLRMDYGNATLFLPDEBGLQHLBTLTTELITKFLAK 297
 QY 299 LSRRVVDVSVRLHMTGTFDLKKTLSYIGVSKIFEBHGDTLTKLAPHRSLKVGSAVHRAEL 358
 Db 298 SSRVSVVRRPKLSISTYDLKPLGKLGITQVSDNADLSGITGEQPLKASQHLHRAVL 357
 QY 359 KMDEGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKI PSYLVFGKIVNP 411
 Db 358 TIDRGTEAAGATYMEIIPMSLPSITLDRPFLFVIYSHKISPLFVGKIVDP 410

RESULT 7
 JX0267
 alpha-1-antiprotease S-1 precursor - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
 C/Accession: JX0267
 R/Saito, A.; Sinohara, H.
 J. Biochem. 113, 456-461, 1993
 A/Title: Rabbit plasma alpha-1-antiprotease S-1: cloning, sequencing, expression, and
 A/Reference number: JX0267; MUID:93293795; PMID:8514734
 A/Accession: JX0267
 A/Molecule type: mRNA
 A/Residues: 1-413 <SAI>
 A/Cross-references: UNIPROT:Q07299; UNIPARC:UPI0000086E35; GB:D16104; NID:g286191; PIDN:A
 A/Experimental source: liver
 A/Note: Part of this sequence, including the amino end of the mature protein, was confir
 C/Superfamily: serpin
 C/Keywords: glycoprotein
 F.1-24/Domain: signal sequence #status predicted <SIG>
 F.25-413/Product: alpha-1-antiprotease S-1 #status experimental <MAT>
 F.65,102,266/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.5%; Score 778.5; DB 2; Length 413;
 Best Local Similarity 37.8%; Pred. No. 3.1e-46;
 Matches 156; Conservative 95; Mismatches 157; Indels 5; Gaps 2;

QY 1 MNPTLGAIPLAVLLTVKGLKPSFSPRYKALSEVQGMKQMAAKELARQNMDLGFKLL 60
 Db 1 MPFSVSRAL---LLLAGIGCLLPGLADEAQETAVSSHEDHPACHRIAPSLAEFALSLY 57
 QY 61 KKLAFYNGRNIFLSPISITAFSMLCLGAQDSTLDEIKQG--FNFRKMPKDLHEGFHY 118
 Db 58 REVAHESNTNTNIFSPVISALAFAMLSLGAAGDTHTVLEGLKFNLTETAAQIHDFGRH 117
 QY 119 IIEHLQKTDKLSIGNTLFIIDRLQPORKEFLDANKFSAETILTNFONLEMAQKQIN 178
 Db 118 LHTVNRPDSELOLAAGNALVHENTLQHKFLEDAKQLQSEAFVDFPDPEQAKTKIN 177
 QY 179 DFIQKTHGKINLNIENIDPGTWMLANYIFPRARKHEDPNVTKEDDFLEKNSSVKY 238
 Db 178 SHVEKGTGRKIVDLVQELDARTLLALVNVYFFKGMKEKPEPENTKEDDFVDAATTVRV 237
 QY 239 PMFRSGIYGVYDDKLSCTILFIYQKNTAIFILPDEGQLKLEKGLQVDTFSRKTL 298
 Db 238 PMMSRLGMVYKFCSTLASVTLRMDYGNATLFLPDEBGLQHLBTLTTELITKFLAK 297
 QY 299 LSRRVVDVSVRLHMTGTFDLKKTLSYIGVSKIFEBHGDTLTKLAPHRSLKVGSAVHRAEL 358
 Db 298 SSRVSVVRRPKLSISTYDLKPLGKLGITQVSDNADLSGITGEQPLKASQHLHRAVL 357
 QY 359 KMDEGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKI PSYLVFGKIVNP 411
 Db 358 TIDRGTEAAGATFVGIMPSLPSISVTFDRPFLFVIYSHKISPLFVGKIVDP 410

RESULT 8
 A54968
 alpha-1-antitrypsin precursor - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 05-Oct-2004
 C/Accession: A54968
 R/Ray, B.K.; Gao, X.; Ray, A.
 J. Biol. Chem. 269, 22080-22086, 1994
 A/Title: Expression and structural analysis of a novel highly inducible gene encoding a
 A/Reference number: A54968; MUID:94350954; PMID:8071331
 A/Accession: A54968
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-413 <RAY>
 A/Cross-references: UNIPROT:Q28666; UNIPARC:UPI00000876E0; GB:L12139; NID:g405551; PIDN:J
 C/Superfamily: serpin

Query Match 36.4%; Score 775.5; DB 2; Length 413;
 Best Local Similarity 37.3%; Pred. No. 5e-46;
 Matches 154; Conservative 100; Mismatches 154; Indels 5; Gaps 2;

QY 1 MNPTLGAIPLAVLLTVKGLKPSFSPRYKALSEVQGMKQMAAKELARQNMDLGFKLL 60
 Db 1 MPFSVSRAL---LLLAGIGCLLPGLADEAQETAVSSHEDHPACHRIAPSLAEFALSLY 57
 QY 61 KKLAFYNGRNIFLSPISITAFSMLCLGAQDSTLDEIKQG--FNFRKMPKDLHEGFHY 118
 Db 58 REVAHESNTNTNIFSPVISALAFAMLSLGAAGDTHTVLEGLKFNLTETAAQIHDFGRH 117
 QY 119 IIEHLQKTDKLSIGNTLFIIDRLQPORKEFLDANKFSAETILTNFONLEMAQKQIN 178
 Db 118 LHTVNRPDSELOLAAGNALVHENTLQHKFLEDAKQLQSEAFVDFPDPEQAKTKIN 177
 QY 179 DFIQKTHGKINLNIENIDPGTWMLANYIFPRARKHEDPNVTKEDDFLEKNSSVKY 238
 Db 178 SHVEKGTGRKIVDLVQELDARTLLALVNVYFFKGMKEKPEPENTKEDDFVDAATTVRV 237
 QY 239 PMFRSGIYGVYDDKLSCTILFIYQKNTAIFILPDEGQLKLEKGLQVDTFSRKTL 298
 Db 238 PMMSRLGMVYKFCSTLASVTLRMDYGNATLFLPDEBGLQHLBTLTTELITKFLAK 297

QY	299	LSRRRVDSVPRIMHTGTDTDLAKKTSYIGVSKISFEHGGDLTKLAPHNSLRKGAIVHKAEL	358
		
Db	298	SSRSRYVPRPPKKSISGTYDLKPLVGLQKGIIVFSDNDLSGITEQELKRSQALHRYVL	357
		
QY	359	KMDRGTEGAAGTAQTLPMETPLPVYKIDKPYLLIIYSEKIPSVLFLGIKINP	411
		
Db	358	TIDRGTEGAAGATVAVYVLSMRFQRTFPRPLFYIYSHKVPSPLENGKVDP	410
		

RESULT 5

alpha-1 protease inhibitor 1 - mouse
 N:Alternate names: alpha-1-antitrypsin
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
 C:Accession: I49470, A25495
 R:Berriello, F.; Krauter, K.S.
 Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
 A:Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary divergence
 A:Reference number: I49470; MUID:92052104; PMID:1946354
 A:Accession: I49470
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-413 <RSS>
 A:Cross-references: UNIPROT:P07758; UNIPARC:UPI0000021A6; GB:M75721; NID:G191841; PIDN:AA51624.1; PIDN:Krauter, K.S.; Cifton, B.A.; Hau, M.T.; Powell, D.; Darnell Jr., J.B.
 DNA 5, 29-36, 1986
 A:Title: Isolation and characterization of the alpha-1-antitrypsin gene of mice.
 A:Reference number: A25495; MUID:86163765; PMID:3007061
 A:Accession: A25495
 A:Molecule type: mRNA
 A:Residues: 211-245 'D', 247-322, 'L', 324-403, 'V', 405-413 <KRA>
 A:Cross-references: UNIPARC:UPI000016CC23; GB:M12586; NID:G192092; PIDN:AA51624.1; PIDN:Genetics:
 A:Gene: alpha-1 PI-1
 A:Superfamily: serpin

	Query Match	36.1%	Score 768.5	DB 2	Length 413
	Best Local Similarity	39.4%	Pred. No. 1.5e-45		
	Matches 165	Conservative 85	Mismatches 158	Indels 11	Gaps 5
QY	1	MNPTLGAIPLAVLITLVKGL-LKPSFSPRYKALSEVGCKRMMAKELARONMDLGFK	58		
DB	1	MTPEISMG-----LLLAGLCCLPVFLAEVQGTDSQK-DQSPASHSEIATNTNGDFAIS	54		
QY	59	LKKGLATYNNQGRNIFLSPPLSISTAFSMILCGAOSTLDEIKQG--FNRKRPEDOLHEGF	116		
DB	55	LYRELVAQSNSTSNFFSPVSATATPAMLSIGSKDTHQILGQAFNLTQSEADIHNSF	114		
QY	117	HYIHEFTQKTDKLISGNTLFPIDORLOPORKEFLDEKAPNFYSAETILTNFQNLMAOKQ	176		
DB	115	QHLLQTLNRPDSELOSTGNGLFVNNDLKLVKTELEKKNHYQAEVSVNFAESEAKV	174		
QY	177	INDFISQTHGKINNLIENTDGTVMLLANTIFPRARKHEPDPNVTKEDPFLKONSSV	236		
DB	175	INDFVEKGTOGKLAEAVKLDQDDVVFALANYILTKGKKAKKFPDENTEEAFAHDESTRV	234		
QY	237	KVPMFPRSGIYQVGDGKLSCTIEIPQKRTITFILPDEGKXKHEKGQVDTFSWK	296		
DB	235	KVPMPTLSGMLAHNHCSTLSSVLLMDYAGATNAVFLIPDGGKNOHLEQTLSKELFTL	294		
QY	297	TLLSRVAVDSVPRLHMTGTFDLKKTLSYIGVSKI FEEHGDLTKIAPHRS-LKVGSAVHK	355		
DB	295	LNRRRLAQIHFPRLTISGEYNLKTILMSPLGITRIFFNNGALDSGITEENAPLKLQAIVHK	354		
QY	356	AELKMDRGREGAAGTGAQTLPMETPLVVKIDKRYLLIYSEKPLPSVLFGLKINPGLK	414		
DB	355	AVLTIDTGTGAALVATVLAQVMSMPPLRADHPFLFTEFEHTQSPFLGKAVDPTRK	413		

RESULT 10
I49472

alpha-1-proteinase inhibitor 3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence #revision 02-Jul-1996 #text_change 05-Oct-2004
C:Accession: I49472
R:Boerriello, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A:Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary diver
A:Reference number: I49470; MUID:92052104; PMID:1946554
A:Accession: I49472
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-413 <RES>
A:Cross-references: UNIPROT:000896; UNIPARC:UPI0000028CD4; GB:M75720; NID:g191845; PIDD:J
C:Gene: alpha-1 PI-3
C:Genetics:
C:Superfamily: serpin

Query Match 36.0%; Score 766.5; DB 2; Length 413;
Best Local Similarity 39.4%; Pred. No. 2.1e-45;
Matches 165; Conservative 83; Mismatches 160; Indels 11; Gaps 5;

QY 1 MNPTGLAIFLAVALITLVKGL--LKPSFSPRNKALSEVQGMKQRMAKELARQNMIDGFK 58
DB 1 MTPSISWG----LLTLGLCCLVPSFLAEDVQEDTDSQK--DQSPASHETATYLGDAIS 54
QY 59 LLLKLAIFYNPGRNIFLSPLSISTAFSMLCLGAODSTLDEIKQG--ENFRMPKDLHEGF 116
DB 55 LYRELIVHQSNSTNIFPSPVSIATAFAMLSGSKGDTHTQILEQIGNLTQTSBADIHKSF 114
QY 117 HYTHLTLQTKQDKLSTIGNTLFIDQRLQPRKFLPADACNFSAEITLTPQLLEMAQKQ 176
DB 115 QHLQTLNRPSEQLSTGNGLFVNNDLKLVEKFLBEAKNHYQAEFVSVPFASBEAKV 174
QY 177 INDFISQTHKINNLINIDPGYMLANTYFFPARWGHGEPDNTKEEDFLEKNSV 236
DB 175 INDEVKQTKQKIAEAVKGLQODIVPALANTYLLFGKMKKRPDPENTBEAFHVDSETTV 234
QY 237 KVPNMFSGIYQVGYDVKLSTIIEIPYQKNTALFILDEGKLKHLKGLQVDTFSRMK 296
DB 235 KVPNMTISGMDDVHHCSTLSSVWLLMDYAGNATAVFLLPDDGKMQHLEQLSKELSKFL 294
QY 297 TLSSRVVDSVPRLMATGTDPLDKKTLSTYIGVSKFPEEGDLTKIAPHNS-LKVGELVHK 355
DB 295 LKRRPRRLAQIHFRPRLSISGEYNLKTLMSPGLGTRIFNNGADISGLIEENAPLKSQAVHK 354
QY 356 AELMDERGTEGAAGTGAQTLPMETPLVVKIDPKPYLLIYSEKIPSVLFLGIKIVNPIGK 414
DB 355 AVLMDERTGEAAATVILANVPYMPPIVRPHFPLFIIEHTQSPLEVGKVVDPYHK 413

RESULT 11
I49452
alpha-1-antitrypsin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence #revision 02-Jul-1996 #text_change 05-Oct-2004
C:Accession: I49452
R:Siifers, R.N.; Ledley, F.D.; Reed-Fourquet, L.; Ledbetter, D.H.; Ledbetter, S.A.; Woo, S
Genomics 6, 100-104, 1990
A:Title: Complete cDNA sequence and chromosomal localization of mouse alpha-1-antitrypsin
A:Reference number: I49452; MUID:90152670; PMID:2303352
A:Accession: I49452
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-413 <RES>
A:Cross-references: UNIPROT:P22599; UNIPARC:UPI0000029619; GB:M25529; NID:g191549; PIDD:J
C:Superfamily: serpin

Query Match 35.7%; Score 760.5; DB 2; Length 413;
Best Local Similarity 39.2%; Pred. No. 5.4e-45;
Matches 165; Conservative 88; Mismatches 153; Indels 15; Gaps 7;

QY 1 MNPTGLAIFLAVALITLVKGL--LKPSFSPRNKALSEVQGMKQRMAKELARQNMIDGFK 58
DB 1 MTPSISWG----LLTLGLCCLVPSFLAEDVQEDTDSQK--DQSPASHETATYLGDAIS 54

Db 1 MTPSISWG-----LILLAGLCCLVPSFLAEDVQETDTSQK--DQSPASHETATNLGDPAIS 54
QY 59 LKRLAFYNPGRNIFLSPLSISTASPMLCIGAOSTLDEIKQG--FNFRKMPEDLHGEF 116
Db 55 LYRELVHQSNTNIFSPSVATATPAMLSLGSKGDTHQILEGQFNLQTSSEADIHKSF 114
QY 117 HYIHELQKTDKLSIGNTLPIIDQRLQPKRLEDAKNFYSAETILTNFQNLMAQKQ 176
Db 115 QHLLQTLNRPDSLQSLTGNGLFVNNDLKLVKFLBEAKNHYQAEVPSVAFSEBAKCV 174
QY 177 INDFISQKTHGKINNLENDPGTVMLANYIFPRARKHEPDPNVTKEEDFLEKNSV 236
Db 175 INDFVEKGTQKIVAEAYELDQDTVPALGNLYLFEKGKKKPPDEBTEBAEFHVDKSTTV 234
QY 237 KVPMPFSGIYQVGDGKLSCTILEIPQKNITAFILIPDGSKLHLEKGLQVDTFSRMK 296
Db 235 KVPMPITSGMLDVHNCSTLSWVLLMDYAGNASAVFLPBECKNOHLEQTLNKLIS--K 292
QY 297 TLRS--RRVVDVSVRLMGTGTPDLKKTLSYIGVSKIPEEHGDLTKIAPHRS-LKVGSAV 353
Db 293 ILNRRRLVQIHPRLISIGEYNLKTLMSPLGITRIFPNNGADLSGITENAPKLKSAV 352
QY 354 HKAKLKDDEGTGGAAGTGAQTLPEMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIG 413
Db 353 HKAVLTIDTGTTEAAATVFAVAVMSPILRFPDHPFLFIIEBHQSPIFVGKVDPTH 412
QY 414 K 414
Db 413 K 413

RESULT 12

149473
alpha-1 proteinase inhibitor 4 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C/Accession: 149473
R/Bortolillo, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A/Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary divergence
A/Reference number: 149470; MUID:32052104; PMID:1946354
A/Accession: 149473
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-413 <RES>
A/Cross-references: UNIPROT:Q00897; UNIPARC:UPI0000003B4C; GB:M75718; NID:g191847; PIDN:
C/Genetics:
A/Gene: alpha-1 PI-4
C/Superfamily: serpin

Query Match 35.6%; Score 758.5; DB 2; Length 413;
Best Local Similarity 39.4%; Pred. No. 7.4e-45;
Matches 166; Conservative 87; Mismatches 153; Indels 15; Gaps 7;

QY 1 MNEPLGATFLAVLLTVKGF--LKPSFSPNNYKALSEVQGMKQMAKELARQNMDDGFK 58
Db 1 MTPSISWG-----LILLAGLCCLVPSFLAEDVQETDTSQK--DQSPASHETATNLGDPAIR 54
QY 59 LKRLAFYNPGRNIFLSPLSISTASPMLCIGAOSTLDEIKQG--FNFRKMPEDLHGEF 116
Db 55 LYRELVHQSNTNIFSPSVATATPAMLSLGSKGDTHQILEGQFNLQTSSEADIHKSF 114
QY 117 HYIHELQKTDKLSIGNTLPIIDQRLQPKRLEDAKNFYSAETILTNFQNLMAQKQ 176
Db 115 QHLLQTLNRPDSLQSLTGNGLFVNNDLKLVKFLBEAKNHYQAEVPSVAFSEBAKCV 174
QY 177 INDFISQKTHGKINNLENDPGTVMLANYIFPRARKHEPDPNVTKEEDFLEKNSV 236
Db 175 INDFVEKGTQKIVAEAYELDQDTVPALGNLYLFEKGKKKPPDEBTEBAEFHVDKSTTV 234
QY 237 KVPMPFSGIYQVGDGKLSCTILEIPQKNITAFILIPDGSKLHLEKGLQVDTFSRMK 296
Db 235 KVPMPITSGMLDVHNCSTLSWVLLMDYAGNASAVFLPBECKNOHLEQTLNKLISQF- 293

QY 297 TLRSRRVVD--VSVPRLMGTGTPDLKKTLSYIGVSKIPEEHGDLTKIAPHRS-LKVGSAV 353
Db 294 -ILNRRRSDAQIHPRLISIGENYNLKTLMSPLGITRIFPNNGADLSGITENAPKLKSAV 352
QY 354 HKAKLKDDEGTGGAAGTGAQTLPEMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIG 413
Db 353 HKAVLTIDTGTTEAAATVQVATYSPPIRVFDPHPFLFIIEBHQSPIFVGKVDPTH 412
QY 414 K 414
Db 413 K 413

RESULT 13

149471
alpha-1 proteinase inhibitor 2 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C/Accession: 149471
R/Bortolillo, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A/Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary divergence
A/Reference number: 149470; MUID:32052104; PMID:1946354
A/Accession: 149471
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-402 <RES>
A/Cross-references: UNIPROT:P22599; UNIPARC:UPI000016CBEA; GB:M75716; NID:g191843; PIDN:
C/Genetics:
A/Gene: alpha-1 PI-2
C/Superfamily: serpin

Query Match 35.5%; Score 756; DB 2; Length 402;
Best Local Similarity 40.1%; Pred. No. 1.1e-44;
Matches 159; Conservative 85; Mismatches 145; Indels 8; Gaps 5;

QY 23 PSFSPRYKALSEVQGMKQMAKELARQNMDDGFKLLKRLAFYNPGRNIFLSPLSISTA 82
Db 9 PSFLAEDVQETDTSQK--DQSPASHETATNLGDPAISLYRELVHQSNTNIFSPSVATATA 67
QY 83 PSMLCIGAOSTLDEIKQG--FNFRKMPEDLHGEFYIHELQKTDKLSIGNTLFI 140
Db 68 FANLSLGSKGDTHQILEGQFNLQTSSEADIHKSFQHLLQTLNRPDSLQSLTGNGLFV 127
QY 141 DQRLQPKRLEDAKNFYSAETILTNFQNLMAQKQINDFISQKTHGKINNLENDPGT 200
Db 128 NNDLKLVKFLBEAKNHYQAEVPSVAFSEBAKVINDFVEKGTQKIVAEAYELDQDT 187
QY 201 VMLLANYIFPRARKHEPDPNVTKEEDFLEKNSVYVPMFSGIYQVGDGKLSCTIL 260
Db 188 VFLANLYLFEKGKKKPPDEBTEBAEFHVDKSTTVAVPMMLSGMLDVHNCSTLSWV 247
QY 261 EIPYQKNITAFILIPDGSKLHLEKGLQVDTFSRMKTLRS--RRVVDVSVRLMGTGTPD 318
Db 248 LMDYAGNASAVFLPBECKNOHLEQTLNKLIS--KILNRRRLVQIHPRLISISDYN 305
QY 319 LKKTLSYIGVSKIPEEHGDLTKIAPHRS-LKVGSAVHKAKLKDDEGTGGAAGTGLP 377
Db 306 LKTLMSPLGITRIFPNNGADLSGITENAPKLKSAVHKAVLTIDTGTTEAAATVFAVAVP 365
QY 378 METPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIG 414
Db 366 MSMPILRFPDHPFLFIIEBHQSPIFVGKVDPTHK 402

RESULT 14

S60036
alpha-1-antitrypsin precursor - golden hamster
N/Alternate names: alpha-1-antitrypsinase
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 05-Oct-2004
C/Accession: S60036

R:Nakatsu, T.; Suzuki, Y.; Yoshida, K.; Shinohara, H.
 Blochm. Biochem. Acta 1263, 245-248, 1995
 A:Title: Molecular cloning and sequence analysis of cDNA encoding plasma alpha-1-antipryc
 A:Reference number: S60036; MID:96004896; PMID:7548212
 A:Accession: S60036
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-413 <NA>
 A:Cross-references: UNIPROT:P92727; UNIPARC:UPI0000067E5; EMBL:D49709; NID:G1088432; PI
 A:Note: the source is designated as Syrian hamster
 C:Superfamily: serpin
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-413/Product: alpha-1-antitrypsin #status predicted <MAT>

Query Match 35.4%; Score 753; DB 2; Length 413;
 Best Local Similarity 38.7%; Pred. No. 1,8e-44;
 Matches 161; Conservative 87; Mismatches 158; Indels 10; Gaps 4;

QY 1 MNPTGLAIFLAVLLTVKGL--LKPSFSPNNYKALSEVQGWKQMAKELARQNMDLGFK 58
 DB 1 MKPSISMGILL-----LAGLCLVPSFLAEDAQETDASKQDQHQAACKIAPMLADPSFN 55
 QY 59 LKKGLAFYNGRNIPLSLISTAFSMLCIGADSTLDEIKQ--GRNFRKMPKDLHEGR 116
 DB 56 LKRELHQSNTNIPFSVPISIAFAFMLSIGTKGVHTQTLEGLGNLIEIAEAHVHKGK 115
 QY 117 HYIHELTKQTDKLSIGNTLFIQRLQPKRFLKEDAKNFYSAETILTFFONLEMAOKQ 176
 DB 116 HNLLQTFNRPDNELOLTGNGLFTHNNLKYDKFLKLVKNDYSEAFVNFPTSEAKKY 175
 QY 177 INDFISQKTHGKINNLINENIDPGTMLLANYIFFRARKHEFPDNTKEDPFLKRNSSV 236
 DB 176 INGFEVKGTOGKIVDLVKDLDKDTVALVYIPEFKGKKRFPDADNTEADPFVDDKTTYV 235
 QY 237 KYPMMERSGIYQGVGDKSCITLLEIPYQKNTAIFILPDEGLKHLKGLQVDTFSRMK 296
 DB 236 KQPMMSRLQMFDPHVVSTLSSWVLLMDYLGNAATAIPLPDGKQHLBQTLNKEITIGKFL 295
 QY 297 TLLSRVVDVSVRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSIKVGEAVHKA 356
 DB 296 KDRHRSAAVNHFFKLSISGYNLKTLADPLGITOVFSNGADLSGITEDVPLKQKAVHKA 355
 QY 357 ELKMDERGTEGAAGTQTLPMETPLVVKIDKPYLLIYS-EKIPSVLFGKIIVNP 411
 DB 356 VLTIDERGTEAAGATFMEIIPMSVPEVFNPSPIAIHYDRQAKSPLFVGKVVDP 411

RESULT 15

S11320
 serine protease inhibitor 3 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
 C:Accession: S11320; S08100
 R:Pages, G.; Rouayenc, J.F.; le Cam, G.; Mariller, M.; le Cam, A.
 Eur. J. Biochem. 190, 385-391, 1990
 A:Title: Molecular characterization of three rat liver serine-protease inhibitors affect
 A:Reference number: S11318; MID:90306038; PMID:1694763
 A:Accession: S11320
 A:Molecule type: mRNA
 A:Residues: 1-408 <PAG>
 A:Cross-references: UNIPARC:UPI0000167956; EMBL:X16359; NID:G57234; PTDN:CA34408.1; PID
 R:le Cam, A.
 submitted to the EMBL Data Library, August 1989
 A:Reference number: S08099
 A:Accession: S08100
 A:Molecule type: mRNA
 A:Residues: 1-366 <LE>
 A:Cross-references: UNIPARC:UPI0000176300; EMBL:X16359
 C:Superfamily: serpin

Query Match 35.1%; Score 747.5; DB 2; Length 408;
 Best Local Similarity 40.6%; Pred. No. 4.2e-44;
 Matches 151; Conservative 79; Mismatches 133; Indels 9; Gaps 5;

QY 48 LARQNMDLGFKLKKLAFYNGRNIPLSLISTAFSMLCIGADSTLDEIKQ--FNFR 105
 DB 37 LMSINDPAPSLYKGLALNPHNGVPSPLISAAALAVSLGAKGSMEEILGLKFNLT 96
 QY 106 KMPKDLHEGRNIYIHELTKQTDKLSIGNTLFIQRLQPKRFLKEDAKNFYSAETILT 165
 DB 97 EYETETIHHGFGHILQRLSQPRDEIQISTGNMLFIKRLQVLAEPQEKAKALYQAEAF7A 156
 QY 166 NPNQLEMAOKQINDFISQKTHGKINNLINENIDPGTMLLANYIFFRARKHEFPDNTKED 225
 DB 157 DFOQSRKAKLLINDVSKOTQGIQGLITNLAKTSMVLVNIYFPGKMKVPPDPDPTQ 216
 QY 226 EDFLEKNSSVKPMFRSGIYQGV--DDKLSCTTLEIPYQKNTAIFILPDEGLKHL 283
 DB 217 SEFYSGKRSSVAVPMKLEDL--TTPYRDEBLNCTVLELKTGNASALFILPDQGMQGV 275
 QY 284 EKGQVDTFSRMKTLISRVVD--VSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIA 342
 DB 276 EASLQPETLRMRWDSIRPSMIDELVLPKFSISADVNLBVLPELGIKEVFSIQADLSGIT 335
 QY 343 PHRSIKVGEAVHKAELKMDERGTEGAAGTQTLPMET--PLVVKIDKPYLLIYSEKI 399
 DB 336 GDDKLVVFOVHKAVDVAETGEAATAVGKFPKSAKLDPLILAFDPPLMITSDET 395
 QY 400 PSVLFGKIIVNP 411
 DB 396 AIAPIAKIIFNP 407

Search completed: March 31, 2006, 09:50:51
 Job time : 42 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:43:04 ; Search time 233 Seconds
(without alignments)
1253.600 Million cell updates/sec

Title: US-10-664-356-1562

Perfect score: 2130
Sequence: 1 MNPTGLAIFLAVLLTVKGL.....YSEKIPSVLFLKIVNPITGK 414

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:.*
1: uniprot_sprotc:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2130	100.0	414	2 Q81W75	HUMAN
2	1406	66.0	411	2 Q8R421	RAT
3	1380	64.8	413	2 Q7TWF5	MOUSE
4	1378	64.7	413	2 Q9CQ32	MOUSE
5	1369	64.3	413	2 Q6P6M3	MOUSE
6	876.5	41.2	422	2 Q6STX0	XENLA
7	857	40.2	431	2 Q66KX6	XENLA
8	857	40.2	433	2 Q9Y1B8	XENLA
9	841	39.5	436	2 Q5M911	XENTR
10	827	38.8	426	2 Q8JTA6	SPHPU
11	792	37.2	396	1 A1AT	CERAB
12	790	37.1	418	1 A1AT	PONPY
13	787	36.9	409	1 A1AT	PAPAN
14	785.5	36.9	413	2 Q28665	RABIT
15	785	36.9	411	1 A1AT	RAT
16	785	36.9	418	1 A1AT	HUMAN
17	785	36.9	418	2 Q53XB8	HUMAN
18	782	36.7	406	1 A1AT	MERUN
19	780.5	36.6	413	1 A1AT	RABIT
20	778.5	36.5	413	2 Q07298	RABIT
21	775.5	36.4	413	2 Q28666	RABIT
22	772.5	36.3	456	2 Q62663	RABIT
23	772	36.2	411	2 Q9TPE1	BOVIN
24	768.5	36.1	413	1 A1AT1	MOUSE
25	766.5	36.0	413	1 A1AT3	MOUSE
26	766	36.0	417	2 Q5J801	BOVIN
27	764	35.9	415	2 Q9GMA6	PIG
28	763	35.8	421	1 A1AT	PIG
29	762.5	35.8	413	1 A1AT2	MOUSE
30	761	35.7	412	1 A1AT	CALCN
31	758.5	35.6	413	1 A1AT4	MOUSE

32	753	35.4	413	1 A1AT	MESAU
33	752.5	35.3	412	1 A1AT6	MOUSE
34	752.5	35.3	420	2 Q60552	MESAU
35	752	35.3	421	1 A1AT2	HORSE
36	745.5	35.0	413	2 Q8VC41	MOUSE
37	745	35.0	418	1 CP13	RAT
38	743.5	34.9	418	1 CP16	RAT
39	742.5	34.9	413	1 A1AT5	MOUSE
40	742.5	34.9	413	2 Q545P1	MOUSE
41	742	34.8	416	1 A1AT	BOVIN
42	740	34.7	413	1 ALMS	SPETR
43	737.5	34.6	416	1 CP11	RAT
44	735	34.5	445	1 SP43F	MOUSE
45	733	34.4	413	2 Q76HP0	TAMSI

ALIGNMENTS

RESULT 1
Q81W75 HUMAN PRELIMINARY; PRT; 414 AA.
AC Q81W75;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 13-SEP-2005 (TREMblrel. 31, Last annotation update)
DE Serine (or cysteine) proteinase inhibitor, clade A (Alpha-1
DB antiproteinase, antitrypsin), member 12 (OU-64) (Visceral adipose-
DE specific SERPIN).
GN Name=SERPIN12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
CX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebin T.B., Toshtyuk S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalka U., Smalllee D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
PT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RG NIH MGC Project;
RU Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Chen S., Guo J.H., Yu L.,
RU Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
[4]
RN NUCLEOTIDE SEQUENCE.
RA Hida K., Wada J., Zhang H.,
RU Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

-1- SIMILARITY: Belongs to the serpin family.
 CC EMBL: BC040857; AA040857.1; -; mRNA.
 DR EMBL: AY177692; AA018649.1; -; mRNA.
 DR EMBL: AY326420; AAP89384.1; -; mRNA.
 DR HSSP: P01009; 10MB.
 DR Ensembl: ENSG00000165953; Homo sapiens.
 DR HGN: HGNC:18359; SERPINA12.
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR000215; Prot_inh_serpin.
 DR Pfam: PF00079; Serpin; 1.
 DR SMART: SM00093; SERPIN; 1.
 KM Serpin.
 SQ SEQUENCE 414 AA; 47175 MW; 5C70F1AB5935661C CRC64;
 Query Match 100.0%; Score 2130; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 2,3e-143;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNPTGLAIFLAVLLTVKGLKPSFSPRNKALSEVQGMKQMAAKELARQNDLGFKLL 60
 DB 1 MNPTGLAIFLAVLLTVKGLKPSFSPRNKALSEVQGMKQMAAKELARQNDLGFKLL 60
 QY 61 KCLAFNPGRNIFLSPLSTASTASMLCLGADSTLDEIKGFNFRKMPKDLHEGFHYII 120
 DB 61 KCLAFNPGRNIFLSPLSTASTASMLCLGADSTLDEIKGFNFRKMPKDLHEGFHYII 120
 QY 121 HELTQKTQDLKLSIGNTLFDQRLQPKRFLBDANKFYSAETILTNFQNLMAKOINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFDQRLQPKRFLBDANKFYSAETILTNFQNLMAKOINDF 180
 QY 181 ISQKTHGKINNLINENIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVP 240
 DB 181 ISQKTHGKINNLINENIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVP 240
 QY 181 ISQKTHGKINNLINENIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVP 240
 DB 181 ISQKTHGKINNLINENIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVP 240
 QY 241 MFRSGIYGVYGDKLSCTLLEIPYOKNITAFILPDEGKLKHLKGLQVDTFSRMKTLIS 300
 DB 241 MFRSGIYGVYGDKLSCTLLEIPYOKNITAFILPDEGKLKHLKGLQVDTFSRMKTLIS 300
 QY 301 RRVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTFLAPRSLKYGEAVHKAELNM 360
 DB 301 RRVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTFLAPRSLKYGEAVHKAELNM 360
 QY 361 DERGTGGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLKIVNPICK 414
 DB 361 DERGTGGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLKIVNPICK 414
 RESULT 2
 QBR421_RAT PRELIMINARY; PRT; 411 AA.
 ID QBR421;
 AC QBR421;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Visceral adipose tissue specific SERPIN.
 GN Name=Serpin12; Synonym=Vaepin;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OK NCBI_TaxId=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=OLETF; TISSUE=Visceral adipose;
 RA Hida K., Wada J., Zhang H., Shikata K., Makino H.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBD databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL: AF245398; AAL99574.1; -; mRNA.
 DR HSSP: P01008; 1ATN.
 DR Ensembl: ENSRNOG0000009710; Rattus norvegicus.
 DR RGD: 708485; Serpin12.
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR000295; Prot_inh_leerp2.

DR InterPro: IPR000215; Prot_inh_serpin.
 DR Pfam: PF00079; Serpin; 1.
 DR PRINTS: PR00780; LEUSERPINII.
 DR SMART: SM00093; SERPIN; 1.
 KM Serpin.
 SQ SEQUENCE 411 AA; 47527 MW; 29FA271FP8C8A2D CRC64;
 Query Match 66.0%; Score 1406; DB 2; Length 411;
 Best Local Similarity 62.8%; Pred. No. 8.8e-92;
 Matches 258; Conservative 84; Mismatches 69; Indels 0; Gaps 0;
 QY 1 MNPTGLAIFLAVLLTVKGLKPSFSPRNKALSEVQGMKQMAAKELARQNDLGFKLL 60
 DB 1 MNPTGLAIFLAVLLTVKGLKPSFSPRNKALSEVQGMKQMAAKELARQNDLGFKLL 60
 QY 61 KCLAFNPGRNIFLSPLSTASTASMLCLGADSTLDEIKGFNFRKMPKDLHEGFHYII 120
 DB 61 KCLAFNPGRNIFLSPLSTASTASMLCLGADSTLDEIKGFNFRKMPKDLHEGFHYII 120
 QY 121 HELTQKTQDLKLSIGNTLFDQRLQPKRFLBDANKFYSAETILTNFQNLMAKOINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFDQRLQPKRFLBDANKFYSAETILTNFQNLMAKOINDF 180
 QY 181 ISQKTHGKINNLINENIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVP 240
 DB 181 ISQKTHGKINNLINENIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVP 240
 QY 181 ISQKTHGKINNLINENIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVP 240
 DB 181 ISQKTHGKINNLINENIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVP 240
 QY 241 MFRSGIYGVYGDKLSCTLLEIPYOKNITAFILPDEGKLKHLKGLQVDTFSRMKTLIS 300
 DB 241 MFRSGIYGVYGDKLSCTLLEIPYOKNITAFILPDEGKLKHLKGLQVDTFSRMKTLIS 300
 QY 301 RRVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTFLAPRSLKYGEAVHKAELNM 360
 DB 301 RRVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTFLAPRSLKYGEAVHKAELNM 360
 QY 361 DERGTGGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLKIVNPICK 411
 DB 361 DERGTGGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLKIVNPICK 411
 RESULT 3
 Q7TME5_MOUSE PRELIMINARY; PRT; 413 AA.
 ID Q7TME5;
 AC Q7TME5;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Visceral adipose-specific SERPIN.
 GN Name=Serpin12;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OK NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Swiss Webster;
 RA Hida K., Wada J., Zhang H.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBD databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL: AY326419; AAP88383.1; -; mRNA.
 DR HSSP: P01008; 1ATN.
 DR MGI: MGI:1915304; Serpin12.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR InterPro: IPR000295; Prot_inh_leerp2.
 DR InterPro: IPR000215; Prot_inh_serpin.
 DR Pfam: PF00079; Serpin; 1.
 DR PRINTS: PR00780; LEUSERPINII.
 DR SMART: SM00093; SERPIN; 1.
 DR PROSITE: PS00284; SERPIN; 1.
 KM Serpin.
 SQ SEQUENCE 413 AA; 47674 MW; E52B3B08C2DD418F CRC64;

Query Match 64.8%; Score 1380; DB 2; Length 413;
 Best Local Similarity 61.3%; Pred. No. 6.3e-90;
 Matches 253; Conservative 85; Mismatches 75; Indels 0; Gaps 0;

QY 1 MNPFLGALPLVALVLTYYGKLLKSPSPRYNYSALSEVQCMKORMAAKSLARQNDLGRKLL 60
 DB 1 MTRMLDGLPLAGLLTYKGLLQDDADAPMDSPRVQVEMRGKQDARQLARINMEFGKLL 60

QY 61 KKLAFYNGRNIFLPSLSTAFPSMLCLGADSTLDELKOGFNPKRBEKHLGHPYII 120
 DB 61 QRLASNSPRGNIFLPSLSTAFPSMLCLGADSTLDELKOGFNPKRBEKHLGHPYII 120

QY 121 HELTQTKQDLKLSIGNTLFLIDQLQPKRKLKEDAKNFYSATLITLNFONLEMAKQINDF 180
 DB 121 HKLNOETEDTKMNLGNLFPMDQKLRPOQRFLNLAKNYYDADMDVLTTFODLENTQKIDNRY 180

QY 181 ISQTKHKKINNLNLENDIPGVMLLANTIFPRAKKHEFDNPVTKSEDFLEKNSVYVPM 240
 DB 181 ISRTHSRIRKNMVSIDPGVTMLTNYTFPRGMQVFEFDPKQTEBEFFLEKGTIVYPM 240

QY 241 MPRSGIYQVGVDDKLSCTILIEIPYOKNITAFILPDGKCLKHEKGLQVDFPSWKTLIS 300
 DB 241 MPRGGLYDAVYDQSLCTILIEIPRGKITATFVLPDNGKCLKHEKGLQVADIFPAKWSKLS 300

QY 301 RRVVDSVPLHMTGTFEDLKKTLISYGVSKIPEHGDLTAKIAPRSLKVGSAVAKELKM 360
 DB 301 KRVVDVWVPLRISSTYTNMKKVLRLGISKIFPENGDLTIRSHRSKVGSAVAKELKM 360

QY 361 DEGTGCACTGAGTILPMETPLVYKIDKPYLLILSKIRPSVLFLGKIYVPIG 413
 DB 361 DEKMGGAAGAGTILPMETPRHMKDPRFLMILYENFMPSMIFLARIYDPSG 413

RESULT 4
 Q9C032 MOUSE PRELIMINARY; PRT; 413 AA.

ID Q9C032; 01-JUN-2001 (TrEMBLrel. 17, Created)
 AC Q9C032; 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched
 DE library, clone:463419J12 product:hypothetical Serpins containing
 DE protein, full insert sequence (Mus musculus 17 days embryo head cDNA,
 DE RIKEN full-length enriched library, clone:330000F13
 DE product:hypothetical Serpins containing protein, full insert
 DE sequence).

GN Name=Serpin12;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Scudlitz F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustlisch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima M., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamakawa I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schoenbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Choithia C., Corbani L.B., Cousine S.,
 RA Dalla B., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 RA Grimmond S., Gustlisch S., Hirokawa N., Jackson I.D., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Whitlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshew-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hltrozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiyagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-Format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
 RA Adachi J., Aizawa K., Akihira S., Akiyama T., Arai A., Aono H.,
 RA Atakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL: BC078523; AA078523.1; -, mRNA.
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR000295; ProtInhLeasp2.
 DR InterPro: IPR000215; ProtInhSerpin.
 DR Pfam: PF00079; Serpin_1.
 DR PRINTS: PRO0780; LEUSERPINIT.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Serpin.
 KW SEQUENCE 431 AA; 48870 MW; 41ADB4EC6B6ED57 CRC64;
 SQ
 Query Match 40.2%; Score 857; DB 2; Length 431;
 Best Local Similarity 42.6%; Pred. No. 1.3e-52;
 Matches 159; Conservative 91; Mismatches 121; Indels 2; Gaps 1;
 QY 41 ORMAAKELARONNDLGFKLKLAFAFNPGRNIFLSPISSTAFSMCLGADSTLDEIKQ 100
 DB 57 ESMPCIKIAPNNAHPSFLYRKLAADNPTEINFLSPVISTATAMSLGAKGQTLKQITE 116
 QY 101 G--FNRKMPKEDLHGEFYIHELTOQTQDKLSIGNTLFTIDRLQPKRPLEDAKNFY 158
 DB 117 GLSFNTTISEEIHKGFOHLMLNDPSEMGQNSGNALFIDKDPQIIQKFEADAKQFY 176
 QY 159 SAEITLTNQNLMAKQKINDPISQTHGKINNLINENIDPGVMTLANTYFFPAKAKHEF 218
 DB 177 EAEPSVTDHNTBEAKQINSYAEKKTNGKITELTSTVEKTLVINYTFRGWKEKPF 236
 QY 219 DPNVTEKEDPFLEKSSSVKPMFRSGIYQVGYDDKLSITLIEIPYOKNTAIFILPDG 278
 DB 237 EKENTVDGEFHDYKDVVYVPMHKGKMTNVAYDQGLCTVLMFPGKNAITLFIIPDGG 296
 QY 279 KLEHLEKGLQVDTFSRMTLLSRVVDVSPRLMTGTDPDKKTLSTYIGVSKI FEEHGD 338
 DB 297 KLRQVEALELTPVVKSMRKIFRRRSVNLTPKPSISATLDLVKELTGLVDFVDSGSL 356
 QY 339 TKIAPRSLKVGAEVAKELKNDERGTGCAAGTQTLPMETPLVVKIDKPYLLIYSK 398
 DB 357 SGTEAPPLRVSAVKAVALSIDETGETEAGVGMELPMVMSRIFENKPFLLIYYGQ 416
 QY 399 IPSVLFLGIKINP 411
 DB 417 TRSNYPMGRINMP 429
 RESULT 8
 Q5Y1B8_XENLA PRELIMINARY; PRT; 433 AA.
 AC Q5Y1B8;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Alpha-1-antitrypsinase.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 NCBI_TaxID=8355;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=liver;
 RA Yoshida K., Suzuki Y., Sinohara H.;
 RT "Cloning and comparative sequence analysis of Xenopus laevis alpha1-
 RT antitrypsinase."
 RL J. Biochem. Mol. Biol. Biophys. 3:59-63(1999).
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL: AB014091; BAA36581.1; -, mRNA.
 DR HSPF; P01009; IOMB.

DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR000295; ProtInhLeasp2.
 DR InterPro: IPR000215; ProtInhSerpin.
 DR Pfam: PF00079; Serpin_1.
 DR PRINTS: PRO0780; LEUSERPINIT.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
 DR Serpin.
 KW SEQUENCE 433 AA; 48909 MW; 4E37C65317BCF2AC CRC64;
 SQ
 Query Match 40.2%; Score 857; DB 2; Length 433;
 Best Local Similarity 42.6%; Pred. No. 1.3e-52;
 Matches 159; Conservative 87; Mismatches 125; Indels 2; Gaps 1;
 QY 41 ORMAAKELARONNDLGFKLKLAFAFNPGRNIFLSPISSTAFSMCLGADSTLDEIKQ 100
 DB 59 ESMPCIKIAPNNAHPSFLYRKLAADNPTEINFLSPVISTATAMSLGAKGQTLKQITE 118
 QY 101 G--FNRKMPKEDLHGEFYIHELTOQTQDKLSIGNTLFTIDRLQPKRPLEDAKNFY 158
 DB 119 GLSFNTTISEEIHKGFOHLMLNDPSEMGQNSGNALFIRNNKLIKQFLEVDKNIY 178
 QY 159 SAEITLTNQNLMAKQKINDPISQTHGKINNLINENIDPGVMTLANTYFFPAKAKHEF 218
 DB 179 GSAFSTDFQNAEAKQINSYAEKKTNGKITELTSTVEKTLVINYTFRGWKEKPF 238
 QY 219 DPNVTEKEDPFLEKSSSVKPMFRSGIYQVGYDDKLSITLIEIPYOKNTAIFILPDG 278
 DB 239 DEELTQDGIFFYDENTNTVYVPMHKGKMTNVAFDRKGLCTVQIIPKGNASALFIIPDGG 298
 QY 279 KLEHLEKGLQVDTFSRMTLLSRVVDVSPRLMTGTDPDKKTLSTYIGVSKI FEEHGD 338
 DB 299 KLRQVEALELTPVVKSMRKIFRYQSVLSIPKPSISAEIDLIEVFKGLGVTDFVDSGSL 358
 QY 339 TKIAPRSLKVGAEVAKELKNDERGTGCAAGTQTLPMETPLVVKIDKPYLLIYSK 398
 DB 359 TGIVEAKKLVSAVKAVALSIDETGETEAAATTAETIEMMLPENVNRPFLIITYDME 418
 QY 399 IPSVLFLGIKINP 411
 DB 419 TKTHTLFLGRINMP 431
 RESULT 9
 Q5M911_XENTR PRELIMINARY; PRT; 436 AA.
 AC Q5M911;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE LOC496632 protein (Fragment).
 GN Name=LOC496632;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus; Silurana.
 NCBI_TaxID=8364;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhut N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bork S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosha S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 FAhey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Touchman J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE-whole body;
 RC Klein S., Gerhard D.S.;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL; BC087750; AAH87750.1; -, mRNA.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR000295; Prot_inh_serpin.
 DR InterPro; IPR00215; Prot_inh_serpin.
 DR Pfam; PF00079; Serpin_1.
 DR PRINTS; PR00780; LRU SERPIN1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
 KM Serpin.
 FT NON_TER
 SQ SEQUENCE 436 AA; 49692 MW; 07EB4D2A7446A34B CRC64;
 Query Match 39.5%; Score 841; DB 2; Length 436;
 Best Local Similarity 42.1%; Pred. No. 1,8e-51;
 Matches 157; Conservative 94; Mismatches 120; Indels 2; Gaps 1;
 QY 41 QMAAKELARONMDLGFLLKLAIFYNPGRNIFLSPISISTAFSMLCIGAOSTLDEIKQ 100
 DB 62 ESMPLKIAFYNNFSGSLVQIAADHPTENIFISPSISITVFMLSGARSNTLNGIIE 121
 QY 101 G--FNPKMKPEKDLHEGFHYIIEHLTQKTODLKISGNTLPIDQLQPKRKLADANFY 158
 DB 122 GLKFNSELTEEBEHKGFQHLHLMLANDPNKVKQLNSGNALFIDKDLQKQFVDSKQFY 181
 QY 159 SAETILNPFONLEMAKOINDFISQKTHKINNLINIDPGVMLLANYIFPRARKHEF 218
 DB 182 EATITSTDFHNTBARTKQIVTANKTKGKITDLSVDEETILVINYIFPGWEKH 241
 QY 219 DPNVTKEDPFLKNSSVKVPMPFRSGIYGVYDCKLSTLILPYOKNTAIFILDEG 278
 DB 242 EKEMTKQGI FHVDENTVTVPMHBRNGMYNVAPEKLGCTVQVPRGNMTALFILDEG 301
 QY 279 KLAHLEKGLQVDFSRKKTILSRVVDVSVPLMTGTFDLKTLSYIGSKI FEEHGL 338
 DB 302 KLAQVEBALAKAVKSKKLFRRKFPVHLTPKLSISATDVLKELSKLGTVDFSSDNL 361
 QY 339 TKLIAPRSLKVGAVHAKELKMDRGTEGAAGTGLPMETPLVVKIDKPYLLIYSEK 398
 DB 362 SGIVDVTPLKVSQAVHVLVVISDTGTGAAGTVMEIVPMLPRILRYNPPVLMIEPT 421
 QY 399 IPSVLFLGIKIVNP 411
 DB 422 LRANLFWGVRVNP 434
 RESULT 10
 Q8JIA6 SPHFU
 ID Q8JIA6 SPHFU PRELIMINARY; PRT; 426 AA.
 AC Q8JIA6;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Alpha-1-antitrypsin (Fragment).
 OS Sphenodon punctatus (Reptalia).
 OC Sphenodontia; Sphenodontia; Sphenodontidae; Sphenodon.
 OC Lepidosaurs; Sphenodontia; Sphenodontidae; Sphenodon.
 OC NCB1_TaxID=8508;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.

RA Metcalf V.J., Brennan S.O., George P.M., Chambers G.K.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL; AF375974; AA046107.1; -, mRNA.
 DR HSSP; P01009; 1BZX.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR000215; Prot_inh_serpin.
 DR Pfam; PF00079; Serpin_1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
 KM Serpin.
 FT NON_TER
 SQ SEQUENCE 426 AA; 48318 MW; 6D75C8737FE70950 CRC64;
 Query Match 38.8%; Score 827; DB 2; Length 426;
 Best Local Similarity 39.6%; Pred. No. 1.7e-50;
 Matches 170; Conservative 93; Mismatches 142; Indels 24; Gaps 6;
 QY 1 MNPTGLAIFLAVALTVKGLKLPSPSPR-----NYKALSEVQGM---KQMAAKEL 48
 DB 1 MPTTLHCLLLAWCAE-----AYSHHPDHQHDHDKQKQTHAGAPPSKMTCHKI 54
 QY 49 ARQNMDLGFLLKLAIFYNPGRNIFLSPISISTAFSMLCIGAOSTLDEIKQ--FNPK 106
 DB 55 APSNADPAFPFYQIAAEADAKVFFSPVISTAFALTLTGAKSTQSQYEGLAFWLLE 114
 QY 107 MPEDDLHEGFHYIIEHLTQKTODLKISGNTLPIDQLQPKRKLADANFYSAETILTN 166
 DB 115 IERBEIHGHRHFWQMSLSDREILNMGNALFIDKDKIPKPLDICKSFYASEGSSN 174
 QY 167 FQNLLEMAKOINDFISQKTHKINNLINIDPGVMLLANYIFPRARKHEFDENVKKE 226
 DB 175 FTSABAEKOINDYIKKTKGELVDLVKNGCDPTWMLVNYILKAKWHPFNATREB 234
 QY 227 DFLKNSSVKVPMPFRSGIYGVYDCKLSTLILPYOKNTAIFILDESKLHLE 284
 DB 235 DFFVDGKTSYKVMNPNDSYNSLHDKKLSCLVQWVDLPQBNVAALFILDESKMQVE 294
 QY 285 KGIQVDFSPKWTLL--SRVVDVSVPLMTGTFDLKTLSYIGSKI FEEHGLTKIA 342
 DB 295 DALSVETLTLEKSLRKERSRHLISIPFISIGYDVKLFRRMGVTEVFPTNQDLSGIT 354
 QY 343 PHRLSKVGAVHAKELKMDRGTEGAAGTGLPMETPLVVKIDKPYLLIYSEKIPSV 402
 DB 355 GSEBLKVSRAVHAKALHANGTEBAKTYIELVPSLPPVVKLNRFFLSYDKTASV 414
 QY 403 LFLGIKIVNP 411
 DB 415 LFWGKIVNP 423
 RESULT 11
 A1AT CERAB
 ID A1AT CERAB STANDARD; PRT; 396 AA.
 AC 000394;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
 DE antiprotease) (Fragment).
 GN Name=SERPIN1;
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Cercopithecidae; Cercopithecinae; Cercopithecus.
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; Cercopithecus.
 OC NCB1_TaxID=9534;
 RX [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RC TISSUE=Kidney;
 RA Yoshida K., Suzuki Y., Yamamoto K., Watanabe M., Shinohara H.;
 RT "Cloning and sequencing of complementary DNAs encoding alpha-2-HS
 RT glycoprotein, alpha-1-antitrypsin, and beta-actin from african green
 RT monkey, Cercopithecus aethiops.";

DR EMBL; D17725; BAA04579.1; -; mRNA.
 DR PIR; S54981; S54981.
 DR HSSP; P01009; 1OMB.
 DR GO; GO:0004867; F_serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR000215; Prot_inh_serpin.
 DR Pfam; PF00079; Serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Serpin; Signal.
 KW SIGNAL.
 FT CHAIN 1 23 Potential.
 FT SEQUENCE 24 413 alpha-1-antiprotease E.
 SQ SEQUENCE 413 AA; 45684 MW; C0E86D6091639E2 CRC64;
 Query Match 36.9%; Score 785.5; DB 2; Length 413;
 Best Local Similarity 37.5%; Pred. No. 1.5e-47;
 Matches 155; Conservative 98; Mismatches 155; Indels 5; Gaps 2;

QY 1 NNPFTGLAIFLAVLLTVKGLKPSFSPRYKALSEVQWKQMAKELARQNMDFGFKLL 60
 DB 1 MPPSVSRAL---LLLAGLGCLPGLADAEQETAVSHEDDHPACHRIAPSLAEFALSLY 57
 QY 61 KKLAFYNGRNIFLSPSLISTAFSMLCIAQDSTLDEIKQG--FNFRKMPKXDLHGFFY 118
 DB 58 KEVAHESNTTNIFPSVSTALAPAMSLGAKGDTHTQVLEGLKFNLTETAEQIHDFGR 117
 QY 119 IIEHLETKTQDRLKLSIGNTFLFDRLQPKRPFLEDAKNFYSAETILTNPQNLMAQKQIN 178
 DB 118 LHTVVRPSELQLAGNMLVHVENKLOHKFLEDAKNLYGSAFLVDFRDPQATKIN 177
 QY 179 DPLSQKTHGKINLLINIDPQTMLLANTYFPPARKHEPDVNTYGEPDFLEKSSVXY 238
 DB 178 SHYKETRCKIKVDLVQELPARKTLALVNVYFFPKGKEKPEPENTKEBDFPHVATTVYV 237
 QY 239 PMWFRSGIYOVGVDDKLSCTILEIPYQKNTAFILPDSKGLGHLKGLQVDFSRWKTLL 298
 DB 238 PMWSRLGMYVHFGSTLSTLAVMDYKGNATFLPLPDSKGLQHLDTLTTELIAFLLAK 297
 QY 299 LSRRAVDVSPRLMHTGTPDLKKTLSYIGVSKIFEEHGDITKAPRSLKGVGAHKAEL 358
 DB 298 SGLRSATVAFPKLSISGTDLKRLKLGITGVFSNNAADLSGTTEOBPLKVSQALHKAVL 357
 QY 359 KNDERGTGGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLAKIYNP 411
 DB 358 TIDERGTGAAGASFVELIPESVDSITLDRPFLVIYSHKISPLFVGKVDVP 410

RESULT 15
 A1AT RAT STANDARD; PRT; 411 AA.
 ID A1AT RAT
 AC P17475; Q6AYZ5;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Alpha-1-antiprotease precursor (Alpha-1-antitrypsin) (Alpha-1-proteinase inhibitor).
 GN Name=Serpin1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath; Muridae; Muridae; Murinae; Rattus.
 OC NCBT_TaxID=10116;
 GN NCBT_TaxID=10116;
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC STRAIN=Miscar; TISSUE=Liver;
 RX MEDLINE=91035351; PubMed=2229024;
 RA Mitsumori Y., Sonda M., Ohkudo K., Takami N., Oda K., Ikehara Y.;
 RT "Molecular cloning and sequencing of the cDNA of rat alpha 1-protease inhibitor and its expression in COS-1 cells";
 RL J. Biochem. 108:230-234 (1990).
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Testis;
 RG NIH - Mammalian Gene Collection (MGC) project;

RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE [MRNA] OF 4-411, PROTEIN SEQUENCE OF 25-57, AND
 RP TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=90148955; PubMed=2302382;
 RA Chao S., Chai K.X., Chao L., Chao J.;
 RT "Molecular cloning and primary structure of rat alpha 1-antitrypsin";
 RL Biochemistry 29:323-329 (1990).
 RN NUCLEOTIDE SEQUENCE [MRNA] OF 188-389.
 RP TISSUE=Liver;
 RA Fink I.L., Bailey T., Morkin E.;
 RL Submitted (Aug-1989) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Inhibitor of serine proteases. The primary target is elastase, but also has a moderate affinity for plasmin and thrombin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- DOMAIN: The reactive center loop (RCL) extends out from the body of the protein and directs binding to the target protease. The protease cleaves the serpin at the reactive site within the RCL, establishing a covalent linkage between the carboxyl group of the serpin reactive site and the serine hydroxyl of the protease. The resulting inactive serpin-protease complex is highly stable (By similarity).
 CC -1- SIMILARITY: Belongs to the serpin family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC EMBL; D00675; BAA00579.1; -; mRNA.
 CC EMBL; BC078824; AAH78824.1; -; mRNA.
 CC EMBL; M3247; AAA0788.1; -; mRNA.
 CC EMBL; X16273; CAA34349.1; -; mRNA.
 DR PIR; A33892; ITRT.
 DR HSSP; P01009; 1OMB.
 DR SMR; P17475; 39-411.
 DR EMBL; ENSRN00000032669; Rattus norvegicus.
 DR InterPro; IPR000215; Prot_inh_serpin.
 DR PANTHER; PTHR11461; Prot_inh_serpin; 1.
 DR Pfam; PF00079; Serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Acute phase; Direct protein sequencing; Glycoprotein;
 KW Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 411 Alpha-1-antiprotease.
 FT REGION 367 386 RCL.
 FT SITE 376 377 Reactive bond.
 FT CARBOHYD 64 64 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 101 101 N-linked (GlcNAc...) (potential).
 FT CONFLICT 265 265 N-linked (GlcNAc...) (potential).
 FT CONFLICT 14 14 A -> G (in Ref. 1 and 2; AAH78824).
 FT CONFLICT 84 84 L -> V (in Ref. 1).
 FT CONFLICT 247 247 M -> I (in Ref. 4).
 FT CONFLICT 248 248 H -> Y (in Ref. 1).
 FT CONFLICT 318 318 K -> N (in Ref. 1).
 FT CONFLICT 322 322 S -> D (in Ref. 4).
 SQ SEQUENCE 411 AA; 46136 MW; B4245CFE21C5C761 CRC64;
 Query Match 36.9%; Score 785; DB 1; Length 411;
 Best Local Similarity 38.8%; Pred. No. 1.6e-47;
 Matches 161; Conservative 94; Mismatches 150; Indels 10; Gaps 5;

QY 1 NNPFTGLAIFLAVLLTVKGLKPSFSPRYKALSEVQWKQMAKELARQNMDFGFKLL 60
 DB 1 MAPSISRGILLIALALC---CLAPSLADAGE--TTSQDDGSPYTRKISSNADAFSLY 56
 QY 61 KKLAFYNGRNIFLSPSLISTAFSMLCIAQDSTLDEIKQG--FNFRKMPKXDLHGFFY 118

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:51:09 ; Search time 167 Seconds
(without alignment)
1035.816 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTLGAIPLAVLITVKG.....YSEKIPSVLFGKIVNPIGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2130	100.0	414	3	US-09-755-665-14 Sequence 14, App1
2	2130	100.0	414	3	US-09-755-665-55 Sequence 55, App1
3	2130	100.0	414	3	US-09-755-665-56 Sequence 56, App1
4	2130	100.0	414	4	US-10-168-425-12 Sequence 12, App1
5	2130	100.0	414	4	US-10-629-248-14 Sequence 14, App1
6	2130	100.0	414	4	US-10-629-248-55 Sequence 55, App1
7	2130	100.0	414	4	US-10-629-248-56 Sequence 56, App1
8	2130	100.0	415	4	US-10-012-542-134 Sequence 134, App
9	2130	100.0	415	4	US-10-115-123-134 Sequence 134, App
10	2130	100.0	415	4	US-10-800-834-134 Sequence 134, App
11	2114	99.2	431	4	US-10-276-774-2202 Sequence 2202, Ap
12	1798	84.4	361	3	US-09-755-665-57 Sequence 57, App1
13	1798	84.4	361	4	US-10-629-248-57 Sequence 57, App1
14	840	39.5	377	4	US-10-037-417-66 Sequence 67, App1
15	840	39.5	377	4	US-10-023-634-87 Sequence 87, App1
16	837	39.3	377	4	US-09-823-187-31 Sequence 31, App1
17	786	36.9	418	5	US-10-741-600-1216 Sequence 1216, Ap
18	786	36.9	418	5	US-10-741-600-1217 Sequence 1217, Ap
19	786	36.9	418	5	US-10-741-600-1218 Sequence 1218, Ap
20	786	36.9	418	5	US-10-741-600-1219 Sequence 1219, Ap
21	786	36.9	418	5	US-10-741-600-1220 Sequence 1220, Ap
22	786	36.9	418	5	US-10-741-600-1221 Sequence 1221, Ap
23	786	36.9	418	5	US-10-741-600-1222 Sequence 1222, Ap
24	785	36.9	363	3	US-09-755-665-58 Sequence 58, App1
25	785	36.9	363	4	US-10-629-248-58 Sequence 58, App1
26	785	36.9	394	4	US-09-993-180-6 Sequence 6, App1
27	785	36.9	394	4	US-10-025-514-2 Sequence 2, App1

28	785	36.9	394	4	US-10-365-738-1 Sequence 1, App1
29	785	36.9	394	6	US-11-077-276-2 Sequence 2, App1
30	785	36.9	395	5	US-10-914-863-2 Sequence 2, App1
31	785	36.9	418	4	US-10-037-340-286 Sequence 286, App
32	785	36.9	418	4	US-10-411-037-22 Sequence 22, App1
33	785	36.9	418	4	US-10-411-026-22 Sequence 22, App1
34	785	36.9	418	4	US-10-410-962-22 Sequence 22, App1
35	785	36.9	418	4	US-10-411-049-22 Sequence 22, App1
36	785	36.9	418	4	US-10-408-765A-2304 Sequence 2304, Ap
37	785	36.9	418	4	US-10-410-930-22 Sequence 22, App1
38	785	36.9	418	4	US-10-410-997-22 Sequence 22, App1
39	785	36.9	418	4	US-10-411-012-22 Sequence 22, App1
40	785	36.9	418	4	US-10-287-994-22 Sequence 22, App1
41	785	36.9	418	4	US-10-410-913-22 Sequence 22, App1
42	785	36.9	418	5	US-10-410-980-22 Sequence 22, App1
43	785	36.9	418	5	US-10-971-461-15 Sequence 15, App1
44	785	36.9	418	5	US-10-410-897-22 Sequence 22, App1
45	785	36.9	418	5	US-10-492-261-22 Sequence 22, App1

ALIGNMENTS

RESULT 1
US-09-755-665-14 Application US/09755665
Sequence 14, App1
Patent No. US20020107186A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallion, Bruce B.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OR INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-14
Query Match 100.0%; Score 2130; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPTLGAIPLAVLITVKGILKPSFSPRYKALSEVGWQMAAKELARQNDLGFKL 60
DB 1 MNPTLGAIPLAVLITVKGILKPSFSPRYKALSEVGWQMAAKELARQNDLGFKL 60
QY 61 KKAAPNPGNITLSPISISTAFSMCLGQDSITLBEIKGFPRKPEDLHGFYIT 120
DB 61 KKAAPNPGNITLSPISISTAFSMCLGQDSITLBEIKGFPRKPEDLHGFYIT 120
QY 121 HELTQTKQDIAKLSIGNTLFDQRLQPKFLDPAKAFYSATLITLTFQNLMAQKQND 180
DB 121 HELTQTKQDIAKLSIGNTLFDQRLQPKFLDPAKAFYSATLITLTFQNLMAQKQND 180
QY 181 ISQTKGKINLLENIDPGTMLLANYIFFRARWKIEPDNVTKEEDFLEKNSVYKPM 240
DB 181 ISQTKGKINLLENIDPGTMLLANYIFFRARWKIEPDNVTKEEDFLEKNSVYKPM 240
QY 241 MFRSGIYQGVYDQKLSCTILIEPYQKNITAFILPDGKIKHLEKGLQVTFPRMKTLLS 300
DB 241 MFRSGIYQGVYDQKLSCTILIEPYQKNITAFILPDGKIKHLEKGLQVTFPRMKTLLS 300
QY 301 RRVVDVSVPLHMTGTFTDLKTLSTYGVSKIFREHGLTKIAPHRLKVGEAVHKAELKM 360

```

Db      301 RRVADVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSLSKVGEAVHKAELKM 360
Qy      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414
Db      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

```

RESULT 2

```

US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhiradas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-55

```

```

Query Match      100.0%; Score 2130; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 NMPTGLAIFLAVLITVKGILKPSFSPRNYKALSEVQWKQMAAKELARQNMNDLGFKLL 60
Db      1 NMPTGLAIFLAVLITVKGILKPSFSPRNYKALSEVQWKQMAAKELARQNMNDLGFKLL 60
Qy      61 KKLAFNPGRNIFLSPLSISTAFSMCLGADSTLDEIKQGFNFRMPKEDLHEGFHYII 120
Db      61 KKLAFNPGRNIFLSPLSISTAFSMCLGADSTLDEIKQGFNFRMPKEDLHEGFHYII 120
Qy      121 HELTQTDKLKISIGNTLFIQRLQPKRKLFDANKFYSAETILTNFQNLMAQKQINDF 180
Db      121 HELTQTDKLKISIGNTLFIQRLQPKRKLFDANKFYSAETILTNFQNLMAQKQINDF 180
Qy      181 ISQKTHGKINNLIENIDPGTVMILANYIFFRARWKHEFPDNTKEDFLEKNSSVKVP 240
Db      181 ISQKTHGKINNLIENIDPGTVMILANYIFFRARWKHEFPDNTKEDFLEKNSSVKVP 240
Qy      241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGLKHLKGLQVDTFSRWKTLIS 300
Db      241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGLKHLKGLQVDTFSRWKTLIS 300
Qy      301 RRVADVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSLSKVGEAVHKAELKM 360
Db      301 RRVADVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSLSKVGEAVHKAELKM 360
Qy      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414
Db      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

```

RESULT 3

```

US-09-755-665-56
; Sequence 56, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhiradas K.
; APPLICANT: Majumder, Kumud

```

```

; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-56

```

```

Query Match      100.0%; Score 2130; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 NMPTGLAIFLAVLITVKGILKPSFSPRNYKALSEVQWKQMAAKELARQNMNDLGFKLL 60
Db      1 NMPTGLAIFLAVLITVKGILKPSFSPRNYKALSEVQWKQMAAKELARQNMNDLGFKLL 60
Qy      61 KKLAFNPGRNIFLSPLSISTAFSMCLGADSTLDEIKQGFNFRMPKEDLHEGFHYII 120
Db      61 KKLAFNPGRNIFLSPLSISTAFSMCLGADSTLDEIKQGFNFRMPKEDLHEGFHYII 120
Qy      121 HELTQTDKLKISIGNTLFIQRLQPKRKLFDANKFYSAETILTNFQNLMAQKQINDF 180
Db      121 HELTQTDKLKISIGNTLFIQRLQPKRKLFDANKFYSAETILTNFQNLMAQKQINDF 180
Qy      181 ISQKTHGKINNLIENIDPGTVMILANYIFFRARWKHEFPDNTKEDFLEKNSSVKVP 240
Db      181 ISQKTHGKINNLIENIDPGTVMILANYIFFRARWKHEFPDNTKEDFLEKNSSVKVP 240
Qy      241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGLKHLKGLQVDTFSRWKTLIS 300
Db      241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGLKHLKGLQVDTFSRWKTLIS 300
Qy      301 RRVADVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSLSKVGEAVHKAELKM 360
Db      301 RRVADVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSLSKVGEAVHKAELKM 360
Qy      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414
Db      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

```

RESULT 4

```

US-10-168-425-12
; Sequence 12, Application US/10168425
; Publication No. US20030124706A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dying Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Darniel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YAO, Monique G.
; APPLICANT: LAU, Preeti
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0003 PCT
; CURRENT APPLICATION NUMBER: US/10/168,425
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903

```

PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO 12
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030124706A1 7257324CD1
US-10-629-425-12

Query Match 100.0%; Score 2130; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLLTVKGLKPSFSPRNKALSEVQGWKQMAAKELARQNDLGFYLL 60
DB 1 MNPTGLAIFLAVLLTVKGLKPSFSPRNKALSEVQGWKQMAAKELARQNDLGFYLL 60
QY 61 KKLAFNPGRNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
DB 61 KKLAFNPGRNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
QY 121 HELTQKQDRLKLSIGNTLFLDQRLQPKRFLKEDAKNFYSATLITNFQNLMAQKQINDF 180
DB 121 HELTQKQDRLKLSIGNTLFLDQRLQPKRFLKEDAKNFYSATLITNFQNLMAQKQINDF 180
QY 181 ISQTHGKINNLLENIDPGTVMLANIIFPRARKHEFDPNVTKEDPFLKNSSVKVP 240
DB 181 ISQTHGKINNLLENIDPGTVMLANIIFPRARKHEFDPNVTKEDPFLKNSSVKVP 240
QY 241 MPRSGIQVGVDDKLSCTIIEIPYQKNITAIFILPDGSKLKHLEKGLQVDFPSWKTLIS 300
DB 241 MPRSGIQVGVDDKLSCTIIEIPYQKNITAIFILPDGSKLKHLEKGLQVDFPSWKTLIS 300
QY 301 RRVVDVSPRLHMTGTFDLKKTLSYIGSVKIFEEHGDLTAKAPRSLKVGSAVHAKELKM 360
DB 301 RRVVDVSPRLHMTGTFDLKKTLSYIGSVKIFEEHGDLTAKAPRSLKVGSAVHAKELKM 360
QY 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSKIDSVLFLGKIIVPIGK 414
DB 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSKIDSVLFLGKIIVPIGK 414

RESULT 5

US-10-629-248-14
Sequence 14, Application US/10629248
Publication No. US20040116671A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce E.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/10/629, 248
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/755, 665
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174, 724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-10-629-248-14

Query Match 100.0%; Score 2130; DB 4; Length 414;

Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLLTVKGLKPSFSPRNKALSEVQGWKQMAAKELARQNDLGFYLL 60
DB 1 MNPTGLAIFLAVLLTVKGLKPSFSPRNKALSEVQGWKQMAAKELARQNDLGFYLL 60
QY 61 KKLAFNPGRNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
DB 61 KKLAFNPGRNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
QY 121 HELTQKQDRLKLSIGNTLFLDQRLQPKRFLKEDAKNFYSATLITNFQNLMAQKQINDF 180
DB 121 HELTQKQDRLKLSIGNTLFLDQRLQPKRFLKEDAKNFYSATLITNFQNLMAQKQINDF 180
QY 181 ISQTHGKINNLLENIDPGTVMLANIIFPRARKHEFDPNVTKEDPFLKNSSVKVP 240
DB 181 ISQTHGKINNLLENIDPGTVMLANIIFPRARKHEFDPNVTKEDPFLKNSSVKVP 240
QY 241 MPRSGIQVGVDDKLSCTIIEIPYQKNITAIFILPDGSKLKHLEKGLQVDFPSWKTLIS 300
DB 241 MPRSGIQVGVDDKLSCTIIEIPYQKNITAIFILPDGSKLKHLEKGLQVDFPSWKTLIS 300
QY 301 RRVVDVSPRLHMTGTFDLKKTLSYIGSVKIFEEHGDLTAKAPRSLKVGSAVHAKELKM 360
DB 301 RRVVDVSPRLHMTGTFDLKKTLSYIGSVKIFEEHGDLTAKAPRSLKVGSAVHAKELKM 360
QY 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSKIDSVLFLGKIIVPIGK 414
DB 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSKIDSVLFLGKIIVPIGK 414

RESULT 6

US-10-629-248-55
Sequence 55, Application US/10629248
Publication No. US20040116671A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce E.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/10/629, 248
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/755, 665
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174, 724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 55
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-10-629-248-55

Query Match 100.0%; Score 2130; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLLTVKGLKPSFSPRNKALSEVQGWKQMAAKELARQNDLGFYLL 60
DB 1 MNPTGLAIFLAVLLTVKGLKPSFSPRNKALSEVQGWKQMAAKELARQNDLGFYLL 60
QY 61 KKLAFNPGRNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
DB 61 KKLAFNPGRNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
QY 121 HELTQKQDRLKLSIGNTLFLDQRLQPKRFLKEDAKNFYSATLITNFQNLMAQKQINDF 180
DB 121 HELTQKQDRLKLSIGNTLFLDQRLQPKRFLKEDAKNFYSATLITNFQNLMAQKQINDF 180

```
Db 121 HELTQKTODLKLSIGNTLFIIDRLQPORKELEDAKNFYSAETILLTNFQNLMAQKQINDF 180
Qy 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRARKHEFDPNVTKEEDFLEKNSSVKVP 240
Db 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRARKHEFDPNVTKEEDFLEKNSSVKVP 240
Qy 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRMKTTLS 300
Db 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRMKTTLS 300
Qy 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTJIAPHRSLSKGEAVHKAELKM 360
Db 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTJIAPHRSLSKGEAVHKAELKM 360
Qy 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414
Db 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414

RESULT 7
US-10-629-248-56
; Sequence 56, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tallon, Bruce B.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/10/629,248
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/114,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 56
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-629-248-56

Query Match 100.0%; Score 2130; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPITGLAIFLAVLLTVKGLKPSFSPRYKALSEVQGMKQMAKELARQNMDDGFKLL 60
Db 1 MNPITGLAIFLAVLLTVKGLKPSFSPRYKALSEVQGMKQMAKELARQNMDDGFKLL 60
Qy 61 KCLAFNPGRNIFLSPLSISTAFSMCLGAQOSTLDEIKOGFNFRKMPKEDLHEGFHYII 120
Db 61 KCLAFNPGRNIFLSPLSISTAFSMCLGAQOSTLDEIKOGFNFRKMPKEDLHEGFHYII 120
Qy 121 HELTQKTODLKLSIGNTLFIIDRLQPORKELEDAKNFYSAETILLTNFQNLMAQKQINDF 180
Db 121 HELTQKTODLKLSIGNTLFIIDRLQPORKELEDAKNFYSAETILLTNFQNLMAQKQINDF 180
Qy 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRARKHEFDPNVTKEEDFLEKNSSVKVP 240
Db 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRARKHEFDPNVTKEEDFLEKNSSVKVP 240
Qy 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRMKTTLS 300
Db 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRMKTTLS 300
Qy 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTJIAPHRSLSKGEAVHKAELKM 360
Db 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTJIAPHRSLSKGEAVHKAELKM 360
Qy 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414
Db 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414
```

```
Qy 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414
Db 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414

RESULT 8
US-10-012-542-134
; Sequence 134, Application US/10012542
; Publication No. US20030044851A1
; GENERAL INFORMATION:
; APPLICANT: Ruden et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
; OTHER INFORMATION: acids
US-10-012-542-134

Query Match 100.0%; Score 2130; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPITGLAIFLAVLLTVKGLKPSFSPRYKALSEVQGMKQMAKELARQNMDDGFKLL 60
Db 1 MNPITGLAIFLAVLLTVKGLKPSFSPRYKALSEVQGMKQMAKELARQNMDDGFKLL 60
Qy 61 KCLAFNPGRNIFLSPLSISTAFSMCLGAQOSTLDEIKOGFNFRKMPKEDLHEGFHYII 120
Db 61 KCLAFNPGRNIFLSPLSISTAFSMCLGAQOSTLDEIKOGFNFRKMPKEDLHEGFHYII 120
Qy 121 HELTQKTODLKLSIGNTLFIIDRLQPORKELEDAKNFYSAETILLTNFQNLMAQKQINDF 180
Db 121 HELTQKTODLKLSIGNTLFIIDRLQPORKELEDAKNFYSAETILLTNFQNLMAQKQINDF 180
Qy 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRARKHEFDPNVTKEEDFLEKNSSVKVP 240
Db 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRARKHEFDPNVTKEEDFLEKNSSVKVP 240
Qy 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRMKTTLS 300
Db 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRMKTTLS 300
Qy 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTJIAPHRSLSKGEAVHKAELKM 360
Db 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTJIAPHRSLSKGEAVHKAELKM 360
Qy 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414
Db 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414
```


Db 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFGKIYVPIGK 414

RESULT 9

```

US-10-115-123-134
; Sequence 134, Application US/10115123
; Publication No. US2003006515A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P202930AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-115-123-134

```

Query Match 100.0%; Score 2130; DB 4; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1.1e-178;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MNPTLGIAFLAVLLTVKGLKPSFSPRNKALSEVQGMKORMAAKELARONMDLGFKLL 60
DB 1 MNPTLGIAFLAVLLTVKGLKPSFSPRNKALSEVQGMKORMAAKELARONMDLGFKLL 60
QY 61 KKLAFYVPGNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPBEKDLHGFYII 120
DB 61 KKLAFYVPGNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPBEKDLHGFYII 120
QY 121 HELTQKODIKLSIGNTLFDQRLQPKRFLBDKAKNYSATLLTNFQNLMAQKQINDF 180
DB 121 HELTQKODIKLSIGNTLFDQRLQPKRFLBDKAKNYSATLLTNFQNLMAQKQINDF 180
QY 181 ISOETGKINNLLENIDPGVTMLLANYIFPRARKHEDPNVTKEEDFLEKSSVYVPM 240
DB 181 ISOETGKINNLLENIDPGVTMLLANYIFPRARKHEDPNVTKEEDFLEKSSVYVPM 240
QY 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIFFLPDEGKLUHLEKGLQVDTFSRWKTLIS 300
DB 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIFFLPDEGKLUHLEKGLQVDTFSRWKTLIS 300
QY 301 RRVAVDVSVPLHMTGTFDLDKKTLSYIGSVKIFEEHGLTIKIAHRSLLKVGSAVHKAELKM 360
DB 301 RRVAVDVSVPLHMTGTFDLDKKTLSYIGSVKIFEEHGLTIKIAHRSLLKVGSAVHKAELKM 360
QY 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFGKIYVPIGK 414
DB 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFGKIYVPIGK 414

```

RESULT 10

US-10-800-834-134
 ; Sequence 134, Application US/10800834
 ; Publication No. US20040146930A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 94 Human Secreted Proteins
 ; FILE REFERENCE: P2029P1D3
 ; CURRENT APPLICATION NUMBER: US/10/800,834
 ; PRIOR FILING DATE: 2004-03-16
 ; PRIOR APPLICATION NUMBER: 10/115,123
 ; PRIOR FILING DATE: 2002-04-04
 ; PRIOR APPLICATION NUMBER: 09/461,325
 ; PRIOR FILING DATE: 1999-12-14
 ; PRIOR APPLICATION NUMBER: PCT/US99/13418
 ; PRIOR FILING DATE: 1999-06-15
 ; PRIOR APPLICATION NUMBER: 60/089,507
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089,508
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089,509
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089,510
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/090,112
 ; PRIOR FILING DATE: 1998-06-22
 ; PRIOR APPLICATION NUMBER: 60/090,113
 ; PRIOR FILING DATE: 1998-06-22
 ; NUMBER OF SEQ ID NOS: 532
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 134
 ; LENGTH: 415
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (415)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 US-10-800-834-134

Query Match 100.0%; Score 2130; DB 4; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1.1e-178;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MNPTLGIAFLAVLLTVKGLKPSFSPRNKALSEVQGMKORMAAKELARONMDLGFKLL 60
DB 1 MNPTLGIAFLAVLLTVKGLKPSFSPRNKALSEVQGMKORMAAKELARONMDLGFKLL 60
QY 61 KKLAFYVPGNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPBEKDLHGFYII 120
DB 61 KKLAFYVPGNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPBEKDLHGFYII 120
QY 121 HELTQKODIKLSIGNTLFDQRLQPKRFLBDKAKNYSATLLTNFQNLMAQKQINDF 180
DB 121 HELTQKODIKLSIGNTLFDQRLQPKRFLBDKAKNYSATLLTNFQNLMAQKQINDF 180
QY 181 ISOETGKINNLLENIDPGVTMLLANYIFPRARKHEDPNVTKEEDFLEKSSVYVPM 240
DB 181 ISOETGKINNLLENIDPGVTMLLANYIFPRARKHEDPNVTKEEDFLEKSSVYVPM 240
QY 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIFFLPDEGKLUHLEKGLQVDTFSRWKTLIS 300
DB 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIFFLPDEGKLUHLEKGLQVDTFSRWKTLIS 300
QY 301 RRVAVDVSVPLHMTGTFDLDKKTLSYIGSVKIFEEHGLTIKIAHRSLLKVGSAVHKAELKM 360
DB 301 RRVAVDVSVPLHMTGTFDLDKKTLSYIGSVKIFEEHGLTIKIAHRSLLKVGSAVHKAELKM 360
QY 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFGKIYVPIGK 414
DB 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFGKIYVPIGK 414

```

RESULT 11

US-10-276-774-2202
; Sequence 2202, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2202
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2202

Query Match 99.3%; Score 2114; DB 4; Length 431;
Best Local Similarity 99.3%; Pred. No. 2.9e-177;

Matches 411; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNFTGLAIFLAVLITVKGILKPSFSPRYKALSEVQGMKQMAKELARQNDLGFKL 60
DB 18 MNFTGLAIFLAVLITVKGILKPSFSPRYKALSEVQGMKQMAKELARQNDLGFKL 77
QY 61 KKLAFNPGRNITLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKDLHEGHYII 120
DB 78 KKLAFNPGRNITLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKDLHEGHYII 137
QY 121 HELTQKODKLSIGNTLFIIDQRLQPKRKLBDKKNFSAETILTNFQNLMAKQINDP 180
DB 138 HELTQKODKLSIGNTLFIIDQRLQPKRKLBDKKNFSAETILTNFQNLMAKQINDP 197
QY 181 ISQKTHGKINNLINIDPGTVMLANIYIFPRARKHGFDPNVTKEEDFLEKNSVYKVP 240
DB 198 ISQKTHGKINNLINIDPGTVMLANIYIFPRARKHGFDPNVTKEEDFLEKNSVYKVP 257
QY 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAIILPDEGKLKLEKGLQVDTFSRMTLLS 300
DB 258 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAIILPDEGKLKLEKGLQVDTFSRMTLLS 317
QY 301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEHGDLTIKIAPHSLSKVGSAVHKALKM 360
DB 318 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEHGDLTIKIAPHSLSKVGSAVHKALKM 377
QY 361 DERGTGAAGTAGTLPMTETPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIGK 414
DB 378 DERGTGAAGTAGTLPMTETPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIGK 431

RESULT 12

US-09-755-665-57
; Sequence 57, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 57

; LENGTH: 361

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)..(361)

; OTHER INFORMATION: wherein Xaa is any amino acid as defined in the

; OTHER INFORMATION: specification

US-09-755-665-57

Query Match 84.4%; Score 1798; DB 3; Length 361;
Best Local Similarity 96.7%; Pred. No. 1.5e-149;

Matches 349; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 54 DLGFKLLKLAFNPGRNITLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKDLH 113
DB 1 DLGFKLLKLAFNPGRNITLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKDLH 60
QY 114 EGFHYIIHELTKQDOKLSIGNTLFIIDQRLQPKRKLBDKKNFSAETILTNFQNLMA 173
DB 61 EGFHYIIHELTKQDOKLSIGNTLFIIDQRLQPKRKLBDKKNFSAETILTNFQNLMA 120
QY 174 QKQINDFISQKTHGKINNLINIDPGTVMLANIYIFPRARKHGFDPNVTKEEDFLEKX 233
DB 121 QKQINDFISQKTHGKINNLINIDPGTVMLANIYIFPRARKHGFDPNVTKEEDFLEKX 180
QY 234 SSYKVPMMFRSGIYQVGYDDKLSCTTLEIPYQKNITAIILPDEGKLKLEKGLQVDTFS 293
DB 181 SSYKVPMMFRSGIYQVGYDDKLSCTTLEIPYQKNITAIILPDEGKLKLEKGLQVDTFS 240
QY 294 RMTLLSRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEHGDLTIKIAPHSLSKVGSAV 353
DB 241 RMTLLSRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEHGDLTIKIAPHSLSKVGSAV 300
QY 354 HRAELMDERGTGAAGTAGTLPMTETPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIG 413
DB 301 HRAELMDERGTGAAGTAGTLPMTETPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIG 360
QY 414 K 414
DB 361 K 361

RESULT 13

US-10-629-248-57
; Sequence 57, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/10/629,248
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(361)

OTHER INFORMATION: wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
us-10-629-248-57

Query Match 84.4%; Score 1798; DB 4; Length 361;
Best Local Similarity 96.7%; Pred. No. 1,5e-149;
Matches 349; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 54 DLGFLKLKLAFLYNGRNIPLSPISISTAFSMLCLGADSTLDEIKOGFNPKMEKOLH 113
DB 1 DLGFLKLKLAFLYNGRNIPLSPISISTAFSMLCLGADSTLDEIKOGFNPKMEKOLH 60
QY 114 EGFYIIHETLQKTDKLSIGNTLFIQDLQOPQKFLBDANKFYSATLITLNFQNLMA 173
DB 61 EGFYIIHETLQKTDKLSIGNTLFIQDLQOPQKFLBDANKFYSATLITLNFQNLMA 120
QY 174 OKQINDPISQKTHGKINLLENIDPGTMLLANTFFPARKHEDPVNTYKSEDFLEKN 233
DB 121 OKQINDPISQKTHGKINLLENIDPGTMLLANTFFPARKHEDPVNTYKSEDFLEKN 180
QY 234 SSVVPMWFRSGIYQVGYDDKLSCTILSIPIYQKNITAFILPDGKLGKLEKGLQVDTFS 293
DB 181 SSVVPMWFRSGIYQVGYDDKLSCTILSIPIYQKNITAFILPDGKLGKLEKGLQVDTFS 240
QY 294 RMTLLSRVVDVSPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLYKLAHRSKLVGEAV 353
DB 241 RMTLLSRVVDVSPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLYKLAHRSKLVGEAV 300
QY 354 HKELKNDERTEGAGTGAQTLPMEITPLVVKIDKPYLLIYSKIPSVLFGKIYVDFIG 413
DB 301 HKELKNDERTEGAGTGAQTLPMEITPLVVKIDKPYLLIYSKIPSVLFGKIYVDFIG 360
QY 414 K 414
DB 361 K 361

RESULT 14
US-10-037-417-66
Sequence 66, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernov, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Paturajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vermet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomil R
APPLICANT: Sciore, Paul
APPLICANT: Billeman, Karen
APPLICANT: Malyskar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles B
APPLICANT: Elsen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037, 417
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018

PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
LENGTH: 377
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Serpin
US-10-037-417-66

Query Match 39.5%; Score 842; DB 4; Length 377;
Best Local Similarity 43.7%; Pred. No. 2.6e-65;
Matches 163; Conservative 86; Mismatches 118; Indels 6; Gaps 4;

QY 45 AKELARQMDLGFLLKLAFLYNGRNIPLSPISISTAFSMLCLGADSTLDEIKQ--GF 102
DB 5 ALKLSANADPAFSLYELVEQNDKNIFFSPVISISALMLSLGAGNATQILEVLGF 64
QY 103 NFRMPKEDLHEGFYIIHETLQKTDKLSIGNTLFIQDLQOPQKFLBDANKFYSAT 162
DB 65 NFRMPKEDLHEGFYIIHETLQKTDKLSIGNTLFIQDLQOPQKFLBDANKFYSAT 124
QY 163 ILTNFQNLMAOKQINDPISQKTHGKINLLENIDPGTMLLANTFFPARKHEDPVNT 222
DB 125 FSVDFSDPEAKQINDVWEKTKQKIDLLKDDSTVLVIVYIYFKGKKKPPBEL 184
QY 223 TKSEDFLEKNSSYKVPWFRSGIYQVGYDDKLSCTILSIPIYQKNITAFILPDG 280
DB 185 TKSEDFLEKNSSYKVPWFRSGIYQVGYDDKLSCTILSIPIYQKNITAFILPDG 244
QY 281 KHLKGLQVDTFSRMTLLSRVVDVSPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLYK 340
DB 245 KHLKGLQVDTFSRMTLLSRVVDVSPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLYK 304
QY 341 IAPHRSLKVGAVHAKELKNDERTEGAGTGAQTLPMEITPLVVKIDKPYLLIYSK 398
DB 305 IAPHRSLKVGAVHAKELKNDERTEGAGTGAQTLPMEITPLVVKIDKPYLLIYSK 364
QY 399 IESVFLGKIYVDFIG 411
DB 365 IESVFLGKIYVDFIG 377

RESULT 15
US-10-023-634-87
Sequence 87, Application US/10023634
Publication No. US2003023639A1
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A
APPLICANT: Coleman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Ballinger, Robert A
APPLICANT: Guo, Xiaojia
APPLICANT: Tchernov, Velizar T
APPLICANT: Shenoy, Suresh G

APPLICANT: U1, U1
APPLICANT: Ellerman, Karen
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patuturajan, Meera
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Gusev, Vladimir Y
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Gangolli, Esha A
APPLICANT: Malvanekar, Uriel M
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glenda
APPLICANT: Miller, Isabelle
APPLICANT: Gerlach, Valerie
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE REFERENCE: 21402-221
CURRENT APPLICATION NUMBER: US/10/023,634
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/256,025
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 60/265,163
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,929
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/274,864
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/276,688
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,880
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/286,409
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/309,246
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/315,600
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 87
LENGTH: 371
TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-634-87

Query Match 39.4%; Score 840; DB 4; Length 371;
Best Local Similarity 43.7%; Pred. No.3.8e-65;
Matches 162; Conservative 86; Mismatches 117; Indels 6; Gaps 4;

QY 47 ELARONMDIGFKLLKLAFFYNPGRNIFLPLSISTAFSMLCIGAODSTLDEIKQ--GFNP 104
DB 1 KLASANADPAFSLYKELVQNPDKNFFSPVISASALAMLSGAKGNTATQILEVLGFNL 60
QY 105 RKMPEKDLHEGRIYIHEITQKTQDKLSTGNTLFDQRLQPKRFLBDKXNFYSATIL 164
DB 61 TETSEKEIHQGFQHLQEBLNRPDTGLQTNALFVDKSLKLDLFLBDSKRLYQSEVPS 120
QY 165 TNFONLEMAOKOINDFISQTHGKINNLEINIDPGVMILANYIFFRARKHGFDPNVTK 224
DB 121 VDFSPDEBAKQOINDBVEKTKQIKDLKDLSDTVLVANITYTKGKKKPFDEPTE 180
QY 225 EEDFLEKNSVYKPMFRSGIYQVGDKLSCTLIEIPYQKNITA-IFILPDE-GKLNH 282
DB 181 EEDFHYDKTIVKPMNQLGTFYFRDEBLNCKVELPYKGNATSMFLIPDEVGKLEQ 240
QY 283 LEKGQVDTFSRWKTLISRRVYDVSVPLAMTGFPLKKTLSYGVSKIPEEHGDLTKTA 342
DB 241 YEAAISPETLRKLEMBEPRVELYLPKFSIEGTYDKOVLANGDTIDLFNSQADLSGIS 300
QY 343 PHSRLKVGAEVKKAEIKMDERGTGGAAGTGAOTLPMETP--LVVKIDKPYLLIYSEKIP 400
DB 301 EBDLKVSKAVKAVKAVLEVBEGTEAATAIGATIVPRSLPELEFTADRPFLLIYDPTG 360

QY 401 SVFLGKIYNP 411
DB 361 SILFMGKVVNP 371

Search completed: March 31, 2006, 09:54:36
Job time : 169 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:52:00 ; Search time 24 Seconds
(without alignments)
525.123 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTLGLAIFLAVLTFVKGL.....YSEKIPSEVFLGKIVNPIGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 3041898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDS5/ptodata/2/pubpaa/US08_NEM_PUB.pep.*
2: /SIDS5/ptodata/2/pubpaa/US06_NEM_PUB.pep.*
3: /SIDS5/ptodata/2/pubpaa/US07_NEM_PUB.pep.*
4: /SIDS5/ptodata/2/pubpaa/PCT_NEM_PUB.pep.*
5: /SIDS5/ptodata/2/pubpaa/US09_NEM_PUB.pep.*
6: /SIDS5/ptodata/2/pubpaa/US10_NEM_PUB.pep.*
7: /SIDS5/ptodata/2/pubpaa/US11_NEM_PUB.pep.*
8: /SIDS5/ptodata/2/pubpaa/US60_NEM_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	842	39.5	377	7	US-11-019-711-66
2	786	36.9	418	6	US-10-995-561-753
3	786	36.9	418	6	US-10-995-561-754
4	786	36.9	418	6	US-10-995-561-755
5	786	36.9	418	6	US-10-995-561-756
6	786	36.9	418	6	US-10-995-561-757
7	786	36.9	418	6	US-10-995-561-758
8	786	36.9	418	6	US-10-995-561-759
9	785	36.9	418	7	US-11-177-506-27
10	785	36.9	418	7	US-11-183-205-22
11	772.5	36.3	350	7	US-11-019-711-67
12	765.5	35.9	415	7	US-11-044-224-19
13	723.5	34.0	406	6	US-10-995-561-748
14	723.5	34.0	406	6	US-10-995-561-749
15	723.5	34.0	406	6	US-10-995-561-750
16	723.5	34.0	406	6	US-10-995-561-751
17	723.5	34.0	406	6	US-10-995-561-752
18	706	33.1	448	7	US-11-072-512-3380
19	703.5	33.0	417	7	US-11-147-047-39
20	703.5	33.0	423	6	US-10-995-561-794
21	703.5	33.0	423	6	US-10-995-561-795
22	703.5	33.0	448	6	US-10-995-561-793
23	690.5	32.4	417	7	US-11-219-282-23
24	663.5	31.2	403	7	US-11-219-282-24
25	575	27.0	444	6	US-10-131-826A-498

26	575	27.0	444	6	US-10-973-115B-498	Sequence 498, App
27	575	27.0	444	7	US-11-071-580-1	Sequence 1, Appl
28	574	26.9	444	6	US-10-995-561-834	Sequence 834, App
29	574	26.9	444	6	US-10-995-561-835	Sequence 835, App
30	574	26.9	484	6	US-10-995-561-833	Sequence 833, App
31	568	26.7	457	6	US-10-995-561-797	Sequence 797, App
32	479.5	22.5	390	7	US-11-219-282-13	Sequence 13, Appl
33	471.5	22.1	390	7	US-11-019-711-65	Sequence 65, Appl
34	471.5	22.1	390	7	US-11-219-282-12	Sequence 12, Appl
35	467	21.9	366	6	US-10-215-245A-2	Sequence 2, Appl
36	466.5	21.9	376	6	US-10-501-035-283	Sequence 283, App
37	465.5	21.9	374	6	US-10-995-561-668	Sequence 668, App
38	465.5	21.9	374	6	US-10-995-561-669	Sequence 669, App
39	463.5	21.8	376	6	US-10-995-561-844	Sequence 844, App
40	463.5	21.8	376	6	US-10-995-561-846	Sequence 846, App
41	463.5	21.8	380	6	US-10-995-561-847	Sequence 847, App
42	463.5	21.8	395	6	US-10-453-372-554	Sequence 554, App
43	460	21.6	397	7	US-11-219-282-11	Sequence 11, Appl
44	457	21.5	397	7	US-11-219-282-9	Sequence 9, Appl
45	447	21.0	379	7	US-11-219-282-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-11-019-711-66
Sequence 66, Application US/11019711
Publication No. US20060009634A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchermey, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Verneet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Radigaru, Muralidhara
APPLICANT: Taupler Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eissen, Andrew J
TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/11/019,711
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US/10/037,417
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231

;; PRIOR FILING DATE: 2001-07-05
;; PRIOR APPLICATION NUMBER: 60/305,060
;; PRIOR FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: 60/318,405
;; PRIOR FILING DATE: 2001-09-10
;; PRIOR APPLICATION NUMBER: 60/318,700
;; PRIOR FILING DATE: 2001-09-12
;; NUMBER OF SEQ ID NOS: 227
;; SOFTWARE: Patent Ver. 2.1
;; SEQ ID NO 66
;; LENGTH: 377
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Serpin
;; OTHER INFORMATION: Consensus Sequence
US-11-019-711-66

Query Match 39.5%; Score 842; DB 7; Length 377;
Best Local Similarity 43.7%; Pred. No. 1e-60;
Matches 163; Conservative 86; Mismatches 118; Indels 6; Gaps 4;

QY 45 AKELAQNNDLGRFKLKLAFVNRGRNIFLSPISISTAFSMCLGAQDSTLDEIKO--GF 102
DB 5 ALKLASANDPAPSLYKELVEQNPDKNIFSPVISISSALAMLSLGAQNTATQILEVGF 64
QY 103 NFRKMPKDLHEGFHYIHELTKOTQDLKLSIGNTLFIDQLOPORKELEDAKNFYSAET 162
DB 65 NLRTSEAHIGHQFQHLDELNRPDGLQTTGNALFVDSKSLDELFELEDSRLVQSEV 124
QY 163 ILTNFQNLMAQKQINDPFSQTHGKINLNINIDPCTVMLANYIFPRARMTGHEPDNV 222
DB 125 PSVDFSDPEBAKQINDVWEKTKQKIKDLKDLDSITVLVAVNIYFKGAKMKKPPDPPEL 184
QY 223 TKREDFLEKNSVVKVPMFRSGIYQVGYDDKSCITLIEPYOKNITA--FEILPDE-GKL 280
DB 185 TEEDDHVDKKTIVKPMNQDGFYFPRDEINLCVLELPHYGNATSMFLIPDEVGKL 244
QY 281 KHEKGLQVDTESRMKTLISRNVVDVSPRLHMTGTFDCLKTSLYIGVSKIFEEHGLTK 340
DB 245 EQVEALSPETLRKMLENNRREVELYLPRFSLEGTYDLKQVLAKGIDTDLFENQADLSG 304
QY 341 IAPHRSLKGAHVAKELKMDERGTGGAAGTGAQTLPMETP--LVVKIDRPYLLIYSEK 398
DB 305 ISEDEDLKYSKAVHKAVLEVDDEGTAAATGAIIVPRSLPRLEFTADRPFLIYDPR 364
QY 399 IPSVLFKGIYVP 411
DB 365 TGSILFMGKVNP 377

RESULT 2
US-10-995-561-753

;; Sequence 753, Application US/10995561
;; Publication No. US20050272054A1
;; GENERAL INFORMATION:
;; APPLICANT: CARGILL, Michele et al.
;; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;; TITLE OF INVENTION: DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001559
;; CURRENT APPLICATION NUMBER: US/10/995,561
;; NUMBER OF SEQ ID NOS: 85702
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 753
;; LENGTH: 418
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-995-561-753

Query Match 36.9%; Score 786; DB 6; Length 418;
Best Local Similarity 42.7%; Pred. No. 4e-56;

Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;

QY 54 DLGFKLLKDLAFVNRGRNIFLSPISISTAFSMCLGAQDSTLDEIKQGFNR--KMPKED 111
DB 56 EFAFSLYRDLAQSNTNIFSPVISIATAPAMLSLSTKADTHDEILEGNLNTETPEAQ 115
QY 112 LHEGFHYIHELTKOTQDLKLSIGNTLFIDQLOPORKELEDAKNFYSAETITNFOULE 171
DB 116 IHEGFQELLRITNQPSQQLTTGNGLFLSEGLKLVDFKLEVDYKCLYHSEAFVNGDTE 175
QY 172 MAQKQINDPFSQTHGKINLNINIDPCTVMLANYIFPRARMTGHEPDNVTEBDFPLE 231
DB 176 EAKQKQINDYVEKGTQKQIVDLVKELDRODVFALVNIIFPKGWERPEFYVDTEBDFHVD 235
QY 232 KNSSVKVPMMFRSGIYQVGYDDKSCITLIEPYOKNITAFILPDEGKLKHEKGLQVDT 291
DB 236 QATTVKVPMMKRLGMNIGHCKKLSWVLMKTLGNATAIPLPDEGKLOHLENELTHDI 295
QY 292 PSRWKTLISRNVVDVSPRLHMTGTFDCLKTSLYIGVSKIFEEHGLTKIAPHRSLKVG 351
DB 296 ITKFLNEDRRSASLHLPKLSITGYDLKSVLGQIGITKVFVSGADLSGVTBAPLKLK 355
QY 352 AVHKAELKMDERGTGGAAGTGAQTLPMETPVLVVKIDRPYLLIYSEKISVLFKGIYVP 411
DB 356 AVHKAVALTIDERGTEAAGAMFLEALPMSIPPEYKFNKPPVFLMIEQNTKSLPFMGKVNP 415
QY 412 IGR 414
DB 416 TQK 418

RESULT 3
US-10-995-561-754

;; Sequence 754, Application US/10995561
;; Publication No. US20050272054A1
;; GENERAL INFORMATION:
;; APPLICANT: CARGILL, Michele et al.
;; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;; TITLE OF INVENTION: DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001559
;; CURRENT APPLICATION NUMBER: US/10/995,561
;; NUMBER OF SEQ ID NOS: 85702
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 754
;; LENGTH: 418
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-995-561-754

Query Match 36.9%; Score 786; DB 6; Length 418;
Best Local Similarity 42.7%; Pred. No. 4e-56;
Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;

QY 54 DLGFKLLKDLAFVNRGRNIFLSPISISTAFSMCLGAQDSTLDEIKQGFNR--KMPKED 111
DB 56 EFAFSLYRDLAQSNTNIFSPVISIATAPAMLSLSTKADTHDEILEGNLNTETPEAQ 115
QY 112 LHEGFHYIHELTKOTQDLKLSIGNTLFIDQLOPORKELEDAKNFYSAETITNFOULE 171
DB 116 IHEGFQELLRITNQPSQQLTTGNGLFLSEGLKLVDFKLEVDYKCLYHSEAFVNGDTE 175
QY 172 MAQKQINDPFSQTHGKINLNINIDPCTVMLANYIFPRARMTGHEPDNVTEBDFPLE 231
DB 176 EAKQKQINDYVEKGTQKQIVDLVKELDRODVFALVNIIFPKGWERPEFYVDTEBDFHVD 235
QY 232 KNSSVKVPMMFRSGIYQVGYDDKSCITLIEPYOKNITAFILPDEGKLKHEKGLQVDT 291
DB 236 QATTVKVPMMKRLGMNIGHCKKLSWVLMKTLGNATAIPLPDEGKLOHLENELTHDI 295
QY 292 PSRWKTLISRNVVDVSPRLHMTGTFDCLKTSLYIGVSKIFEEHGLTKIAPHRSLKVG 351

```

Db      236 1TKPFLNEDRRARASLHLPLSLSTITGYDLSKSVLGQLITVFSNGALBSGVTBEAPLAKSK 355
Oy      352 AVHAKELKNDERGETGAGTGAQTLPMTPLVKIKDKPYLLLIYSEKIPSVLEGIKIVNP 411
         ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      356 AVHKAVLITFDKGTENAAGAMPLEAIPMSIPPEVKFNKPFVPLMIIBQNTKSPLEMGKIVNP 415
Oy      412 ICK 414
         ||| |
Db      416 TOK 418

RESULT 4
US-10-995-561-755
; Sequence 755, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 755
; LENGTH: 418
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-995-561-755

```

[illegible]

```

: FILE REFERENCE: CLO01559
: CURRENT APPLICATION NUMBER: US/10/995,561
: CURRENT FILING DATE: 2004-11-24
: NUMBER OF SEQ ID NOS: 85702
: SOFTWARE: FASTSEQ for Windows Version 4.0.
: SEQ ID NO 756
: LENGTH: 418
: TYPE: prt
: ORGANISM: Homo sapiens
US-10-995-561-756

```

Query Match	36.9%;	Score 786;	DB 6;	Length 418;
Best Local Similarity	42.7%;	Pred. No. 4e-56;		
Matches 155;	Conservative 73;	Mismatches 133;	Indels 2;	Gaps 1

[illegible]

```

RESULT 6
US-10-995-561-757
Sequence 757, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMERPHISMS
TITLE OF INVENTION: CARDIOVASCULAR DISOR
TITLE OF INVENTION: DETECTION AND USES T
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 757
LENGTH: 418
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-757

```

Query Match 36.9%; Score 786; DB 6; Length 418;

BEBL LOCAL SIMILARITY: 42.7%; FIELD NO: 46-56;
 Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;

[illegible]

```

Db      116 IHGFOELRLTTLQPSQOLTTGNGFLFSEGLKLVDRKFLVEDVKULYHSAFTVNFQDTE 175
Qy      172 MAQOQINDFIISQTHGKINNLINIDPGTMLLANYIFPRAKWHEDPVTKEEDFFLE 231
Db      176 BAKKQINDYVEKGTQKIVDLVKELDRLDTPALVNIYFFGKWERPFEVQDTEEDFHVD 235
Qy      232 KNSSVKVPWMPFRSGIYQVGDYDKLSTILBIPYOKNITAIPIIPDEGKLHLEKGLQVDT 291
Db      236 QATTVVPMWKRGLGMFNIOHCKKLSWVLMKYLGNATAIPLIPDEGKLQHLNELTHDI 295
Qy      292 FSRWKTLLSRVVDVSPRLHMTGTFDLKTLSYIGVSKIPEEHGDLTKIAPHRSKVG 351
Db      296 ITRFLENEDRRASLHLPKLSITGYDLKSVLGQGITTKVFSNGADLSGVTBEAPLKSK 355
Qy      352 AVHKAELKNDERGTGGAAGTGLPMTETPLVVKIDKPYLLIYSEKIPSVLFLKIVNP 411
Db      356 AVHKAVALTIDEGKTEAAGMFLBAIPMSIPPEVKFNKPFVFLMIQNTKSPLEFMGKVNP 415
Qy      412 IGR 414
Db      416 TOK 418

```

```

RESULT 7
US-10-995-561-758
/ Sequence 758, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FaSTSeq for Windows Version 4.0
/ SEQ ID NO 758
/ LENGTH: 418
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-995-561-758

Query Match      36.9%; Score 786; DB 6; Length 418;
Best Local Similarity 42.7%; Pred. No. 4e-56;
Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;

Qy      54 DLGFKLLKGLAFYNPGRNIFLSPISITAFPSMLCIGAOSTLDEIKQGNFR--KMPKED 111
Db      56 EFAPSLYRLAHQSNSTNIFSPVSITAFAMLSGTAKDTHDEILGILNFILTEIPEAQ 115
Qy      112 LHGFFYIHELTQKQDLSIGNTLFIIDRLQPORKELEDAKNYSATLITNFQNL 171
Db      116 IHGFOELRLTTLQPSQOLTTGNGFLFSEGLKLVDRKFLVEDVKULYHSAFTVNFQDTE 175
Qy      172 MAQOQINDFIISQTHGKINNLINIDPGTMLLANYIFPRAKWHEDPVTKEEDFFLE 231
Db      176 BAKKQINDYVEKGTQKIVDLVKELDRLDTPALVNIYFFGKWERPFEVQDTEEDFHVD 235
Qy      232 KNSSVKVPWMPFRSGIYQVGDYDKLSTILBIPYOKNITAIPIIPDEGKLHLEKGLQVDT 291
Db      236 QATTVVPMWKRGLGMFNIOHCKKLSWVLMKYLGNATAIPLIPDEGKLQHLNELTHDI 295
Qy      292 FSRWKTLLSRVVDVSPRLHMTGTFDLKTLSYIGVSKIPEEHGDLTKIAPHRSKVG 351
Db      296 ITRFLENEDRRASLHLPKLSITGYDLKSVLGQGITTKVFSNGADLSGVTBEAPLKSK 355
Qy      352 AVHKAELKNDERGTGGAAGTGLPMTETPLVVKIDKPYLLIYSEKIPSVLFLKIVNP 411
Db      356 AVHKAVALTIDEGKTEAAGMFLBAIPMSIPPEVKFNKPFVFLMIQNTKSPLEFMGKVNP 415
Qy      412 IGR 414

```

```

Db      416 TOK 418

RESULT 8
US-10-995-561-759
/ Sequence 759, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FaSTSeq for Windows Version 4.0
/ SEQ ID NO 759
/ LENGTH: 418
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-995-561-759

```

```

Query Match      36.9%; Score 786; DB 6; Length 418;
Best Local Similarity 42.7%; Pred. No. 4e-56;
Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;

Qy      54 DLGFKLLKGLAFYNPGRNIFLSPISITAFPSMLCIGAOSTLDEIKQGNFR--KMPKED 111
Db      56 EFAPSLYRLAHQSNSTNIFSPVSITAFAMLSGTAKDTHDEILGILNFILTEIPEAQ 115
Qy      112 LHGFFYIHELTQKQDLSIGNTLFIIDRLQPORKELEDAKNYSATLITNFQNL 171
Db      116 IHGFOELRLTTLQPSQOLTTGNGFLFSEGLKLVDRKFLVEDVKULYHSAFTVNFQDTE 175
Qy      172 MAQOQINDFIISQTHGKINNLINIDPGTMLLANYIFPRAKWHEDPVTKEEDFFLE 231
Db      176 BAKKQINDYVEKGTQKIVDLVKELDRLDTPALVNIYFFGKWERPFEVQDTEEDFHVD 235
Qy      232 KNSSVKVPWMPFRSGIYQVGDYDKLSTILBIPYOKNITAIPIIPDEGKLHLEKGLQVDT 291
Db      236 QATTVVPMWKRGLGMFNIOHCKKLSWVLMKYLGNATAIPLIPDEGKLQHLNELTHDI 295
Qy      292 FSRWKTLLSRVVDVSPRLHMTGTFDLKTLSYIGVSKIPEEHGDLTKIAPHRSKVG 351
Db      296 ITRFLENEDRRASLHLPKLSITGYDLKSVLGQGITTKVFSNGADLSGVTBEAPLKSK 355
Qy      352 AVHKAELKNDERGTGGAAGTGLPMTETPLVVKIDKPYLLIYSEKIPSVLFLKIVNP 411
Db      356 AVHKAVALTIDEGKTEAAGMFLBAIPMSIPPEVKFNKPFVFLMIQNTKSPLEFMGKVNP 415
Qy      412 IGR 414
Db      416 TOK 418

RESULT 9
US-11-177-506-27
/ Sequence 27, Application US/11177506
/ Publication No. US20060029956A1
/ GENERAL INFORMATION:
/ APPLICANT: Beyer, Wayne F.
/ APPLICANT: Venetta, Thomas M.
/ APPLICANT: Groelke, John W.
/ APPLICANT: Blaesius, Rainer H.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
/ TITLE OF INVENTION: DETECTION OF OVARIAN DISEASE
/ FILE REFERENCE: 46143/294851
/ CURRENT APPLICATION NUMBER: US/11/177, 506
/ CURRENT FILING DATE: 2005-07-08
/ PRIOR APPLICATION NUMBER: 60/586,856
/ PRIOR FILING DATE: 2004-07-09

```


RESULT 11
US-11-019-711-67

Sequence 67, Application US/110197111
Publication No. US2006009634A1

GENERAL INFORMATION:

APPLICANT: Akhuda, Ramesh
APPLICANT: Kedbrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Pattnajjan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine B
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sclore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malayankar, Utiel M
APPLICANT: Rottenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Bolog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Andersson, David W
APPLICANT: Padigaru, Muralidhara

```
/ APPLICANT: Taupier Jr, Raymond J
/ APPLICANT: Miller, Charles E
/ APPLICANT: Eissen, Andrew J
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-235
/ CURRENT APPLICATION NUMBER: US/11/019,711
/ CURRENT FILING DATE: 2004-12-21
/ PRIOR APPLICATION NUMBER: US/10/037,417
/ PRIOR FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: 60/260,018
/ PRIOR FILING DATE: 2001-01-05
/ PRIOR APPLICATION NUMBER: 60/260,360
/ PRIOR FILING DATE: 2001-01-08
/ PRIOR APPLICATION NUMBER: 60/272,411
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: 60/272,817
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/291,186
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 60/303,231
/ PRIOR FILING DATE: 2001-07-05
/ PRIOR APPLICATION NUMBER: 60/305,060
/ PRIOR FILING DATE: 2001-07-12
/ PRIOR APPLICATION NUMBER: 60/318,405
/ PRIOR FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: 60/318,700
/ PRIOR FILING DATE: 2001-09-12
/ NUMBER OF SEQ ID NOS: 227
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 67
/ LENGTH: 360
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Serpin
/ US-11-019-711-67
```

Query Match 36.3%; Score 772.5; DB 7; Length 360;

Best Local Similarity 41.9%; Pred. No. 4.1e-55; Matches 151; Conservative 85; Mismatches 119; Indels 5; Gaps 4;

```
QY 57 FTLKLLKLAAYNPGRNIFLPLSISTAFSMCLGAGDSTLDEIKQ--GFNFRKAPBEKOLH 114
DB 1 FDLYKELAKESPDKNIFSPVISALAMLSIGAKSTATQILEVGFNLTERSEADINQ 60
QY 115 GHHYIIHETLOKTQDKLSIGNTLFTDQLOPQRKLEBDAKNYSMETILTNFQN-LEMA 173
DB 61 GFQHLHLNLRPNKQLQLTANALFVDKSLKLDSEFLBVDKLYGAEVOSVSPDPAEBA 120
QY 174 OKQINDFISQKTHGKINNLINENIDPGVWMLANYIFFRARWKHEPDPNTYKEDPFLBKN 233
DB 121 KQIINDWVKKTKQKIKDLISDIDPTRLVNVNATIFKGMKTPPDPENTRESDFYDET 180
QY 234 SSVKQVPMWRSG-IVGVYDDKLSCTILBIPYQKNITAFILPDEBGLKHLKGLQVDTF 292
DB 181 TTVKQVPMWQGTGRFPRYGRDEBLNCOVLELPYKGNASMLIILPDEGLFVEKALTPETL 240
QY 293 SSWKTLISRRVVDVSPRLMHTGTFPLKKTLSITIGYSKIFEEBGGDTKIAPHRSKLVGA 352
DB 241 KMTYSLTTRRSVELYLPKFKLEISYDLKQVLEGLGTTDFSNKADLSGISEBDTLKYSKV 300
QY 353 VHKAEIKMDERGTEGAAGTGAQTLPME-TPLVYKIDKPYLLLIYSEKIPSVLFLGIKYNP 411
DB 301 VHKAFLEVNEBGETEAAAGTGVITVPSLPPPEFKARPPFLIRDPPTGSIILFMGKYNP 360
```

RESULT 12

US-11-044-224-19

/ Sequence 19, Application US/11044224

/ Publication No. US20060040867A1

/ GENERAL INFORMATION:

/ APPLICANT: Shapito, Leland

```
/ TITLE OF INVENTION: Inhibitors of Serine Protease Activity and Their Use in Methods
/ TITLE OF INVENTION: and Compositions for Treatment of Bacterial Infections
/ FILE REFERENCE: 114232,107
/ CURRENT APPLICATION NUMBER: US/11/044,224
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: 60/123,167
/ PRIOR FILING DATE: 1999-03-05
/ PRIOR APPLICATION NUMBER: 60/137,795
/ PRIOR FILING DATE: 1999-06-03
/ PRIOR APPLICATION NUMBER: 09/518,098
/ PRIOR FILING DATE: 2000-03-03
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 19
/ LENGTH: 415
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ US-11-044-224-19
```

Query Match 35.9%; Score 765.5; DB 7; Length 415;

Best Local Similarity 42.6%; Pred. No. 1.8e-54; Matches 155; Conservative 72; Mismatches 130; Indels 7; Gaps 3;

```
QY 54 DLGFKLLKLAAYNPGRNIFLPLSISTAFSMCLGAGDSTLDEIKQGFNR--KMPERK 111
DB 56 BFAPSLYRQLA---STNIFSPVISATAPAMLSIGTKADTDEILDEGLNFLTIRPEAQ 111
QY 112 LHEGHHYIIHETLOKTQDKLSIGNTLFTDQLOPQRKLEBDAKNYSMETILTNFQNLE 171
DB 112 IHGFGELLRITNPDSQQLTFTGNGLFSEGIKLVDKLEBVDKLYHBAETVNGTDE 171
QY 172 MAOKQ-INDFISQKTHGKINNLINENIDPGVWMLANYIFFRARWKHEPDPNTYKEDPFL 230
DB 172 EAKKQINDYVERKQTKQKIVDLVKELDRDTVALVNIYIFPKGMKRPFEVKTREEDFYV 231
QY 231 EKNSSYKVPWMPFRSGIYGVYDDKLSCTILBIPYQKNITAFILPDEBGLKHLKGLQVD 290
DB 232 DQVTVKVPWMPRLGFMFINQHCCKLSWVLNKKYLGNAATAPFLPDEBGLQHLNENELTD 291
QY 291 TTSRWKTLISRRVVDVSPRLMHTGTFDKLTSYIGVSKIFEEBDDTKIAPHRSKLVG 350
DB 292 ITTKLENEBRRSASLHLPKLSITGYDLSVGLQGIKVPNSGADLSGVTEBAPDKLS 351
QY 351 EAVHKAELKMDERGTEGAAGTGAQTLPMETPLVYKIDKPYLLLIYSEKIPSVLFLGIKYN 410
DB 352 KAVHKAVALTIDKGTGAAGAMFLBAPMSIPPEVYENKRFVLMLEQNTKSLFLFMKQYVN 411
QY 411 PTGK 414
DB 412 PTQK 415
```

RESULT 13

US-10-995-561-748

/ Sequence 748, Application US/10995561

/ Publication No. US20050272054A1

/ GENERAL INFORMATION:

/ APPLICANT: CARGILL, Michele et al.

/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

/ FILE REFERENCE: CL001559

/ CURRENT APPLICATION NUMBER: US/10/995,561

/ CURRENT FILING DATE: 2004-11-24

/ NUMBER OF SEQ ID NOS: 85702

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 748

/ LENGTH: 406

/ TYPE: PRF

/ ORGANISM: Homo sapiens

US-10-995-561-748

Query Match 34.0%; Score 723.5; DB 6; Length 406;

Best Local Similarity 37.0%; Pred. No. 4.6e-51;
Matches 153; Conservative 88; Mismatches 156; Indels 17; Gaps 6;

```
QY 7 LAIFL---AVLTIVKGLKSPSPRYKALSEVQGMKQMAAKELARQNDLGFKLKCL 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MQFLLCVLVLSPOGASLHRRHHPREMKKRV---DLHVGATVAPSSRRDFTFDLYRAL 56
QY 64 AFYNGRNIFLSPSISTAFSMLCLGADSTLDEIKQ--GFNFRKPEKDLHGFHYIHH 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 ASAPASOSIFSPSISMSLAMLSTLGAGSSTKQILLEGGLNLQKSEKELHGFQDLQ 116
QY 122 ELTQKTODLKLSTIGNTLFIIDQRLQPRKPLEDAKNFYSAETILTNPONLEMAQOINDFI 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 ELNQPRDGFOLSLGNALFTDLVVDLQDTFVSAMKTYLADPTFNFRDSAGAMQINDYV 176
QY 182 SOKTHGKINNLINIDPGTVMMLANYIFPARAKHEPDVNTKEBDFLEKNSVYKPYMM 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 AKQTKGKIVDLKNLDSNAVAVINNYIFPAKMETSFNHNKGTQODPYVSETVVRPYMM 236
QY 242 FRSGIYOVGYDDKLSCTILEIPYOKNITAFILPDEGKLHLEKGLQVDTFSRMKTLISR 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 SREDQHYHLLDRNLSCRVGVPGGNATLFIIPSEGMQOVENGSEKTLRKMLKMPFK 296
QY 302 RVDVSVPRILMTGTFDLKTLSYIGVSKIFEEHGDITKJAPRSLKVGAVHKAELKMD 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 ROLELYLPKFSIGSYOLEKVLPSLIGISNFTSHADLSGINSNHNIGVSEWVHKAVEVD 356
QY 362 ERGTGGAAGTGA---QTLPMETPLVVKIDKPYLLIYSEKISVFLGKIYVP 411
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 357 ESGTRAAATGTTFTFRSARLNSORLV-FNRPLMFLVDN---NILFLGKYNRP 406
```

RESULT 14

```
US-10-995-561-749
; Sequence 749, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 749
; LENGTH: 406
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-995-561-749
```

Query Match 34.0%; Score 723.5; DB 6; Length 406;
Best Local Similarity 37.0%; Pred. No. 4.6e-51;
Matches 153; Conservative 88; Mismatches 156; Indels 17; Gaps 6;

```
QY 7 LAIFL---AVLTIVKGLKSPSPRYKALSEVQGMKQMAAKELARQNDLGFKLKCL 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MQFLLCVLVLSPOGASLHRRHHPREMKKRV---DLHVGATVAPSSRRDFTFDLYRAL 56
QY 64 AFYNGRNIFLSPSISTAFSMLCLGADSTLDEIKQ--GFNFRKPEKDLHGFHYIHH 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 ASAPASOSIFSPSISMSLAMLSTLGAGSSTKQILLEGGLNLQKSEKELHGFQDLQ 116
QY 122 ELTQKTODLKLSTIGNTLFIIDQRLQPRKPLEDAKNFYSAETILTNPONLEMAQOINDFI 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 ELNQPRDGFOLSLGNALFTDLVVDLQDTFVSAMKTYLADPTFNFRDSAGAMQINDYV 176
QY 182 SOKTHGKINNLINIDPGTVMMLANYIFPARAKHEPDVNTKEBDFLEKNSVYKPYMM 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 AKQTKGKIVDLKNLDSNAVAVINNYIFPAKMETSFNHNKGTQODPYVSETVVRPYMM 236
QY 242 FRSGIYOVGYDDKLSCTILEIPYOKNITAFILPDEGKLHLEKGLQVDTFSRMKTLISR 301
```

Db 237 SREDQHYHLLDRNLSCRVGVPGGNATLFIIPSEGMQOVENGSEKTLRKMLKMPFK 296

QY 302 RVDVSVPRILMTGTFDLKTLSYIGVSKIFEEHGDITKJAPRSLKVGAVHKAELKMD 361

Db 297 ROLELYLPKFSIGSYOLEKVLPSLIGISNFTSHADLSGINSNHNIGVSEWVHKAVEVD 356

QY 362 ERGTGGAAGTGA---QTLPMETPLVVKIDKPYLLIYSEKISVFLGKIYVP 411

Db 357 ESGTRAAATGTTFTFRSARLNSORLV-FNRPLMFLVDN---NILFLGKYNRP 406

RESULT 15

```
US-10-995-561-750
; Sequence 750, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 750
; LENGTH: 406
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-995-561-750
```

Query Match 34.0%; Score 723.5; DB 6; Length 406;
Best Local Similarity 37.0%; Pred. No. 4.6e-51;
Matches 153; Conservative 88; Mismatches 156; Indels 17; Gaps 6;

```
QY 7 LAIFL---AVLTIVKGLKSPSPRYKALSEVQGMKQMAAKELARQNDLGFKLKCL 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MQFLLCVLVLSPOGASLHRRHHPREMKKRV---DLHVGATVAPSSRRDFTFDLYRAL 56
QY 64 AFYNGRNIFLSPSISTAFSMLCLGADSTLDEIKQ--GFNFRKPEKDLHGFHYIHH 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 ASAPASOSIFSPSISMSLAMLSTLGAGSSTKQILLEGGLNLQKSEKELHGFQDLQ 116
QY 122 ELTQKTODLKLSTIGNTLFIIDQRLQPRKPLEDAKNFYSAETILTNPONLEMAQOINDFI 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 ELNQPRDGFOLSLGNALFTDLVVDLQDTFVSAMKTYLADPTFNFRDSAGAMQINDYV 176
QY 182 SOKTHGKINNLINIDPGTVMMLANYIFPARAKHEPDVNTKEBDFLEKNSVYKPYMM 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 AKQTKGKIVDLKNLDSNAVAVINNYIFPAKMETSFNHNKGTQODPYVSETVVRPYMM 236
QY 242 FRSGIYOVGYDDKLSCTILEIPYOKNITAFILPDEGKLHLEKGLQVDTFSRMKTLISR 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 SREDQHYHLLDRNLSCRVGVPGGNATLFIIPSEGMQOVENGSEKTLRKMLKMPFK 296
QY 302 RVDVSVPRILMTGTFDLKTLSYIGVSKIFEEHGDITKJAPRSLKVGAVHKAELKMD 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 ROLELYLPKFSIGSYOLEKVLPSLIGISNFTSHADLSGINSNHNIGVSEWVHKAVEVD 356
QY 362 ERGTGGAAGTGA---QTLPMETPLVVKIDKPYLLIYSEKISVFLGKIYVP 411
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 357 ESGTRAAATGTTFTFRSARLNSORLV-FNRPLMFLVDN---NILFLGKYNRP 406
```

Search completed: March 31, 2006, 09:55:06
Job time : 25 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocooperation Ltd.

OM protein - protein search, using SW model

Run on: March 31, 2006, 09:54:55 ; Search time 221.073 Seconds
(without alignments)
822.818 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTGLAIPLAVLITVKGK.....YSEKIPSVLFGKIVNPIGK 414

Scoring table: OLIGO4
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 15

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database: A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB	ID
1	414	100.0	414 4 AAU05754
2	414	100.0	414 4 AAB04885
3	414	100.0	414 6 ADA57300
4	414	100.0	414 6 ADA41179
5	414	100.0	414 8 ADN05952
6	414	100.0	415 3 AAY86217
7	414	100.0	415 6 ABO53360
8	353	85.3	414 4 AAM78898
9	310	74.9	358 4 AAU05759
10	181	43.7	431 4 ABB11832
11	181	43.7	431 4 AAM79882
12	129	31.2	140 4 AAM70426

ALIGNMENTS

RESULT 1
AAU05754
ID AAU05754 standard; protein; 414 AA.
XX
AC AAU05754;
XX
DT 24-OCT-2001 (first entry)

XX	Human NOV7 polypeptide.
DE	
XX	
KW	Human, NOV7; AL132990 B; fertility disorder; spermatogenesis; cardiac;
KW	cytostatic; immunomodulatory; antiproliferative; antidiabetic;
KW	cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
KW	pulmonary disorder; haematopoietic disorder; immunological disorder;
KW	inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
KW	wound healing; gene therapy.
OS	
XX	Homo sapiens.
XX	
PN	W0200149729-A2.
XX	
PD	12-JUL-2001.
XX	
PF	05-JAN-2001; 2001WO-US000299.
XX	
PR	06-JAN-2000; 2000US-0174724P.
PR	11-JAN-2000; 2000US-0175434P.
PR	11-JAN-2000; 2000US-0175488P.
PR	12-JAN-2000; 2000US-0175696P.
PR	12-JAN-2000; 2000US-0175743P.
PR	13-JAN-2000; 2000US-0175819P.
PR	07-AUG-2000; 2000US-0223524P.
PR	04-JAN-2001; 2001US-0075566S.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Prayaga SK, Majumder K, Taillon BE, Spaderna SK, Spytek KA;
PI	MacDougall J;
XX	
XX	WPI; 2001-418356/44.
DR	N-PSDB; AAS10874.
XX	
PT	Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
PT	for treating a syndrome associated with a NOVX-associated disorder, e.g.
PT	cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
PT	pulmonary disorder.
XX	
PS	Claim 1, Page 32, 14pp; English.
XX	
CC	The invention relates to nucleic acids encoding NOVX (X being an integer
CC	from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
CC	useful in diagnosing, treating or manufacturing a medicament for a
CC	disease or disorder associated with NOVX e.g. cell proliferation (cancer
CC	and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
CC	disorders (e.g. of spermatogenesis), haematopoietic, immunological,
CC	inflammatory and tumour related disorders, emphysema, cirrhosis, wound
CC	healing. NOVX nucleic acids are also useful in gene therapy. They are
CC	also used for screening for a modulator of activity or of latency or
CC	predisposition to a NOVX-associated disorder. They are also useful for
CC	determining the presence of or predisposition to a NOVX-associated
CC	disorder. The present sequence represents NOV7 (AL132990 B), which has
CC	sequence homology to an unidentified human secreted protein (HWHGUS54)
CC	and to alpha1 anti-trypsin
XX	
SQ	Sequence 414 AA;
XX	
Query Match	100.0%; Score 414; DB 4; Length 414;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 414; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MNPTGLAIPLAVLITVKGKLFSPRYKALSEVQWKORMAKELARQNDLGFKLL 60
DB	1 MNPTGLAIPLAVLITVKGKLFSPRYKALSEVQWKORMAKELARQNDLGFKLL 60
QY	61 KKLAFTNPGRNIFLSPISITAFSMLCIGADSTLDEIKOGFVRKMPKEDLHGGFYII 120
DB	61 KKLAFTNPGRNIFLSPISITAFSMLCIGADSTLDEIKOGFVRKMPKEDLHGGFYII 120
QY	121 HELTORTODLKLSTIGNTLPIDORLPORRKLLEDANKFYSATILLTFONLEMAOKOINDF 180

Db 121 HELTQTKDQLKLSIGNTLFIIDRLQFORKELEDAKNFYSAETLTITNFONLEMAQKQINDF 180
 QY 181 ISOKTHGKINNLINLENDPGTVMLLANYIFPRARKHEFDPNVTKEEDFLEKNSSVKVP 240
 Db 181 ISOKTHGKINNLINLENDPGTVMLLANYIFPRARKHEFDPNVTKEEDFLEKNSSVKVP 240
 QY 241 MFRSGIYQVGYDDKLSCTTLEIPIYQKNITAFILIPDEGKIKHLKGLQVDTFSRWKTLIS 300
 Db 241 MFRSGIYQVGYDDKLSCTTLEIPIYQKNITAFILIPDEGKIKHLKGLQVDTFSRWKTLIS 300
 QY 301 RRNVDSVPRLLMTGTGFDLKKTLISYGVSKIPEEHGDLTKIAPHRSLSKVGSAVHKAELKM 360
 Db 301 RRNVDSVPRLLMTGTGFDLKKTLISYGVSKIPEEHGDLTKIAPHRSLSKVGSAVHKAELKM 360
 QY 361 DERGTGGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYVPIGK 414
 Db 361 DERGTGGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 2

AAE04885

ID AAE04885 standard; protein; 414 AA.

XX AAE04885;

XX 10-SEP-2001 (first entry)

XX Human protease protein-12 (PRTS-12).

Human; protease protein-12; PRTS-12; cytostatic; hypotensive; antiviral;
 gastrointestinal disorder; anorexia; dysphagia; cardiovascular disorder;
 atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;
 Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;
 acquired immune deficiency syndrome; AIDS; neurological disorder; asthma;
 developmental disorder; epithelial disorder; eczema; dementia; noctopia;
 neurological disorder; reproductive disorder; infertility; teratogenesis;
 immunosuppressive; drug screening; actinic keratosis; cardiac; epilepsy;
 anemia; antitumor; gene therapy; antibacterial.

XX Homo sapiens.

XX Key Peptide Location/Qualifiers

XX FT 1..19 /label= Signal_peptide

XX FT Protein 20..414 /note= "Mature human PRTS-12"

XX PN MO200146443-A2.

XX PD 28-JUN-2001.

XX PF 19-DEC-2000; 2000MO-US034811.

XX PR 23-DEC-1999; 99US-0172055P.

XX PR 21-JAN-2000; 2000US-0177334P.

XX PR 28-JAN-2000; 2000US-0178884P.

XX PR 02-FEB-2000; 2000US-0179903P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Yang J, Baughn MR, Burford N, Au-Young J, Lu DM, Reddy R;

XX PI Yue H, Nguyen DB, Tang YT, Yao MG, Lal P,

XX DR WPI; 2001-418080/44.

XX PS N-PSDB; AAD09549.

XX Claim 1; Page 118; 129pp; English.

XX The present sequence is human protease protein (PRTS-12). Human PRTS and

CC its nucleic acid molecule are useful for the diagnosis, treatment and
 CC prevention of disorders associated with increased or decreased expression
 CC of PRTS. Examples of such disorders include, gastrointestinal disorder
 CC such as anorexia, dysphagia; cardiovascular disorder such as
 CC atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as
 CC acquired immune deficiency syndrome (AIDS), asthma; cell proliferative
 CC disorder such as actinic keratosis, cirrhosis; developmental disorder
 CC such as epilepsy, anemia; epithelial disorder such as allergic contact
 CC dermatitis, eczema; neurological disorder such as Alzheimer's disease,
 CC dementia and reproductive disorder such as infertility and teratogenesis.
 CC PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or
 CC transgenic animals (mice or rats) to model human disease. PRTS DNA is
 CC also in useful in gene therapy. PRTS and its immunogenic fragments are
 CC useful for screening libraries of compounds in several drug screening
 CC assays. PRTS is useful for analysing the proteome of a tissue or cell
 CC type

SQ Sequence 414 AA;

Query Match 100.0%; Score 414; DB 4; Length 414;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPPTGLAIFLAVLLTVKGLIKRSPSPNNYKALSEVQWKQMAKELARQNDLGFKLL 60
 Db 1 MNPPTGLAIFLAVLLTVKGLIKRSPSPNNYKALSEVQWKQMAKELARQNDLGFKLL 60
 QY 61 KKLAFNPGRNIFLSPUSISTAFSMCLGADOSTDDEIQGFNPRMPKDLHEGPHYII 120
 Db 61 KKLAFNPGRNIFLSPUSISTAFSMCLGADOSTDDEIQGFNPRMPKDLHEGPHYII 120
 QY 121 HELTQTKDQLKLSIGNTLFIIDRLQFORKELEDAKNFYSAETLTITNFONLEMAQKQINDF 180
 Db 121 HELTQTKDQLKLSIGNTLFIIDRLQFORKELEDAKNFYSAETLTITNFONLEMAQKQINDF 180
 QY 181 ISOKTHGKINNLINLENDPGTVMLLANYIFPRARKHEFDPNVTKEEDFLEKNSSVKVP 240
 Db 181 ISOKTHGKINNLINLENDPGTVMLLANYIFPRARKHEFDPNVTKEEDFLEKNSSVKVP 240
 QY 241 MFRSGIYQVGYDDKLSCTTLEIPIYQKNITAFILIPDEGKIKHLKGLQVDTFSRWKTLIS 300
 Db 241 MFRSGIYQVGYDDKLSCTTLEIPIYQKNITAFILIPDEGKIKHLKGLQVDTFSRWKTLIS 300
 QY 301 RRNVDSVPRLLMTGTGFDLKKTLISYGVSKIPEEHGDLTKIAPHRSLSKVGSAVHKAELKM 360
 Db 301 RRNVDSVPRLLMTGTGFDLKKTLISYGVSKIPEEHGDLTKIAPHRSLSKVGSAVHKAELKM 360
 QY 361 DERGTGGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYVPIGK 414
 Db 361 DERGTGGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 3

ADAS7300

ID ADAS7300 standard; protein; 414 AA.

XX ADAS7300;

XX 20-NOV-2003 (first entry)

XX Human secreted protein #583.

XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;

XX cytostatic; cerebroprotective; neuroprotective; nocitropic;

XX cardiovascular; antiarteriosclerotic; gene therapy;

XX human secreted protein; immune disorder; inflammation;

XX respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;

XX inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;

XX multiple sclerosis; ischaemic brain injury; Parkinson's disease;

XX Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;

XX triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.

XX W02002102994-A2.
 XX 27-DEC-2002.
 XX 19-MAR-2002; 2002WO-US008278.
 XX 21-MAR-2001; 2001US-0277340P.
 XX 19-JUL-2001; 2001US-0306171P.
 XX 13-NOV-2001; 2001US-0331287P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Ruben SM;
 XX WPI; 2003-167512/16.
 XX N-PSDB; ADA56404.
 XX
 XX New human secreted polypeptides and polynucleotides, useful for
 XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
 XX conditions, respiratory disorders, cancers, CNS disorders, or
 XX neurodegenerative disorders.
 XX
 XX Claim 13; SEQ ID NO 1490; 1754pp; English.
 XX
 XX The invention relates to 592 new human secreted polypeptides useful for
 XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
 XX conditions, respiratory disorders, cancers, CNS disorders, or
 XX neurodegenerative disorders, or polypeptides comprising an amino acid
 XX sequence at least 95% identical to the new sequences. The polypeptides,
 XX antibodies or antibody fragments that bind to the polypeptides, nucleic
 XX acids encoding the polypeptides, agonists or antagonists that binds to
 XX the polypeptide, are useful in preparing diagnostic or pharmaceutical
 XX compositions for diagnosing, treating or preventing an e.g. immune
 XX disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 XX nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
 XX allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 XX (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
 XX disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 XX cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
 XX polynucleotides are useful for chromosome identification, chromosome
 XX mapping, for controlling gene expression through triple helix formation
 XX or antisense DNA or RNA, in gene therapy, for identifying individuals
 XX from minute biological samples, in forensic biology, and as hybridization
 XX probes. The polypeptides are useful for molecular weight markers on
 XX sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 XX gels, to raise antibodies, for testing biological activities, and for
 XX treating or preventing neural disorders, immune system disorders,
 XX muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 XX renal, proliferative and/or cancerous diseases. This sequence corresponds
 XX to one of the polypeptide of the invention. Note: The sequence data for
 XX this patent did form part of the printed specification, but was obtained
 XX in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 414 AA;

Query Match 100.0%; Score 414; DB 6; Length 414;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLLTVKGLLKPSFSPRYKALSEVGMORMAKELARONMDLGPKL 60
 DB 1 MNTTGLAIFLAVLLTVKGLLKPSFSPRYKALSEVGMORMAKELARONMDLGPKL 60
 QY 61 KKAFLNPGNNIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKPKPEKDLHEGFYII 120
 DB 61 KKAFLNPGNNIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKPKPEKDLHEGFYII 120
 QY 121 HELTOKTODKLSIGNTLFTIDORLQPKRKLEDAKNYSAFTLLTNQNLNMAQKQINDP 180
 DB 121 HELTOKTODKLSIGNTLFTIDORLQPKRKLEDAKNYSAFTLLTNQNLNMAQKQINDP 180

QY 181 ISQKHGKINNLINIDPGVMTLANIYFFPAARKHEPDPVNTKEDEPFLEKNSSVVKPM 240
 DB 181 ISQKHGKINNLINIDPGVMTLANIYFFPAARKHEPDPVNTKEDEPFLEKNSSVVKPM 240
 QY 241 MFRSGIYQVGYDDKLSCTIIIEIPQKNITAIPIIPDEGKLKHEKGLQVDFSSRWKTLIS 300
 DB 241 MFRSGIYQVGYDDKLSCTIIIEIPQKNITAIPIIPDEGKLKHEKGLQVDFSSRWKTLIS 300
 QY 301 RRVDVSVPLRMHTGTEDLKKTLSYIGVSKIFEEHGLTKAPRRSLKVGSAVKAELKM 360
 DB 301 RRVDVSVPLRMHTGTEDLKKTLSYIGVSKIFEEHGLTKAPRRSLKVGSAVKAELKM 360
 QY 361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLIYSEKISVLFKIVNPIGK 414
 DB 361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLIYSEKISVLFKIVNPIGK 414
 RESULT 4
 ADA41179 standard; protein; 414 AA.
 ID ADA41179
 XX
 XX ADA41179;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX Human secreted protein.
 XX
 XX Human, secreted protein; cancer; hyperproliferative disorder;
 XX rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
 XX anaemia; allergic reaction; asthma; cardiovascular disorder;
 XX wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
 XX antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
 XX vulnetary; cardiant; gene therapy.
 XX
 XX Homo sapiens.
 XX
 XX W02002102993-A2.
 XX 27-DEC-2002.
 XX 19-MAR-2002; 2002WO-US008123.
 XX 21-MAR-2001; 2001US-0277340P.
 XX 19-JUL-2001; 2001US-0306171P.
 XX 13-NOV-2001; 2001US-0331287P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Ruben SM;
 XX WPI; 2003-175238/17.
 XX
 XX Claim 1; SEQ ID NO 1561; 3205pp; English.
 XX
 XX The invention relates to novel genes ADA39629-ADA40565 and proteins
 XX ADA40566-ADA41501 for human secreted proteins, useful for preventing,
 XX treating or ameliorating medical conditions e.g. by protein or gene
 XX therapy. The polypeptides, nucleic acid molecules, antibodies or their
 XX fragments, and agonists or antagonists that bind to the polypeptide are
 XX useful for preparing a diagnostic or pharmaceutical composition for
 XX diagnosing or treating cancer or other hyperproliferative disorder. The
 XX polypeptides and nucleic acid molecules are also useful for detecting
 XX preventing, diagnosing, prognosticating, treating or ameliorating cancer
 XX or other hyperproliferative disorders including neoplasms, autoimmune
 XX disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 XX erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 XX anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 XX thrombocytopenia), allergic reactions including asthma or eczema,

CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 CC range restriction mapping, as molecular weight markers, or as
 CC hybridization or diagnostic probes. The polypeptides and antibodies are
 CC useful for providing immunological probes for differential identification
 CC of the tissues immunohistochemistry assays. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences.

CC Sequence 414 AA;

Query Match 100.0%; Score 414; DB 6; Length 414;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;

Matches 414; Conservative 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLITVKGLIKPSFSPRNKALSEVQGMKQMAAKELARQNMNDLGFKL 60
 DB 1 MNPTGLAIFLAVLITVKGLIKPSFSPRNKALSEVQGMKQMAAKELARQNMNDLGFKL 60
 QY 61 KKLAFNPGRNIFLSPLSISTAFSMCLGAQDSTLDEIKQGFNFRKPEKDLHEGFYII 120
 DB 61 KKLAFNPGRNIFLSPLSISTAFSMCLGAQDSTLDEIKQGFNFRKPEKDLHEGFYII 120
 QY 121 HELTQKTQDLKLSIGNTLFTIDRLQPKFLEDAKNFSAETILTNFQLEMAQKQINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFTIDRLQPKFLEDAKNFSAETILTNFQLEMAQKQINDF 180
 QY 181 ISOCTGKINNLINENIDPGTVMILANYIFPRARKHGFDPNNTKEEDFLEKNSSVKVP 240
 DB 181 ISOCTGKINNLINENIDPGTVMILANYIFPRARKHGFDPNNTKEEDFLEKNSSVKVP 240
 QY 241 MFRSGIYQGYDDKLSCTILIEPYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLIS 300
 DB 241 MFRSGIYQGYDDKLSCTILIEPYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLIS 300
 QY 301 RRVVDVSVRLMHTGTFDCLKTISYGVSKIPEBHGDLTKIAPHRSLKVGSAVHKAELKM 360
 DB 301 RRVVDVSVRLMHTGTFDCLKTISYGVSKIPEBHGDLTKIAPHRSLKVGSAVHKAELKM 360
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIGK 414
 DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIGK 414

RESULT 5
 ADN05952
 ID ADN05952 standard; protein; 414 AA.

AC ADN05952;

DT 01-JUL-2004 (first entry)

DE Antipsoriatic protein sequence #1136.

KM antipsoriatic; gene therapy; psoriasis; diagnosis.

OS Homo sapiens.

PN WO2004028479-A2.

PD 08-APR-2004.

PF 25-SEP-2003; 2003WO-US030907.

PR 25-SEP-2002; 2002US-0414006P.

PA (GENTH) GENENTECH INC.

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PW, Wood WJ;
 PI Wu TD;
 XX WPI; 2004-305105/28.
 DR N-PSDB; ADN05951.

XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.

PS Claim 9; SEQ ID NO 2347; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.

CC Sequence 414 AA;

Query Match 100.0%; Score 414; DB 8; Length 414;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 414; Conservative 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLITVKGLIKPSFSPRNKALSEVQGMKQMAAKELARQNMNDLGFKL 60
 DB 1 MNPTGLAIFLAVLITVKGLIKPSFSPRNKALSEVQGMKQMAAKELARQNMNDLGFKL 60
 QY 61 KKLAFNPGRNIFLSPLSISTAFSMCLGAQDSTLDEIKQGFNFRKPEKDLHEGFYII 120
 DB 61 KKLAFNPGRNIFLSPLSISTAFSMCLGAQDSTLDEIKQGFNFRKPEKDLHEGFYII 120
 QY 121 HELTQKTQDLKLSIGNTLFTIDRLQPKFLEDAKNFSAETILTNFQLEMAQKQINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFTIDRLQPKFLEDAKNFSAETILTNFQLEMAQKQINDF 180
 QY 181 ISOCTGKINNLINENIDPGTVMILANYIFPRARKHGFDPNNTKEEDFLEKNSSVKVP 240
 DB 181 ISOCTGKINNLINENIDPGTVMILANYIFPRARKHGFDPNNTKEEDFLEKNSSVKVP 240
 QY 241 MFRSGIYQGYDDKLSCTILIEPYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLIS 300
 DB 241 MFRSGIYQGYDDKLSCTILIEPYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLIS 300
 QY 301 RRVVDVSVRLMHTGTFDCLKTISYGVSKIPEBHGDLTKIAPHRSLKVGSAVHKAELKM 360
 DB 301 RRVVDVSVRLMHTGTFDCLKTISYGVSKIPEBHGDLTKIAPHRSLKVGSAVHKAELKM 360
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIGK 414
 DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIGK 414

RESULT 6
 AAY86217
 ID AAY86217 standard; protein; 415 AA.

AC AAY86217;

DT 19-APR-2000 (first entry)

DE Human secreted protein HWHGUS4, SEQ ID NO:132.

XX Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy.

OS Homo sapiens.


```

XX XX MO9966041-A1.
XX FN
XX XX 23-DEC-1999.
XX PD
XX XX 15-JUN-1999; 99WO-US013418.
XX PF
XX XX 16-JUN-1998; 98US-0089507P.
XX PR 16-JUN-1998; 98US-0089508P.
XX PR 16-JUN-1998; 98US-0089509P.
XX PR 16-JUN-1998; 98US-0089510P.
XX PR 22-JUN-1998; 98US-0090112P.
XX PR 22-JUN-1998; 98US-0090113P.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA,
PI Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R;
PI Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsoulis G;
XX XX WPI: 2000-106100/09.
XX DR N-PSDB; AAZ97021.
XX PT
XX PT New isolated human genes and the secreted polypeptides they encode,
XX PT useful for diagnosis and treatment of e.g. cancers, neurological
XX PT disorders, immune diseases, inflammation or blood disorders.
XX XX
XX PS Claim 1; Page 389-390; 586pp; English.
XX XX
XX CC AAZ97019 to AAZ97137 represent 94 isolated human secreted protein genes.
XX CC AAZ86215 to AAZ86333 are the secreted proteins encoded by the 94 human
XX CC genes. This sequence represents a fragment of one of the human secreted
XX CC proteins. The genes and their corresponding secreted polypeptides are
XX CC useful for preventing, treating or ameliorating medical conditions, e.g.,
XX CC by protein or gene therapy. Also pathological conditions can be diagnosed
XX CC by determining the amount of the new polypeptides in a sample or by
XX CC determining the presence of mutations in the new genes. Specific uses are
XX CC described for each of the 94 genes, based on which tissues they are most
XX CC highly expressed in, and include developing products for the diagnosis or
XX CC treatment of cancer, tumours, developmental abnormalities and foetal
XX CC deficiencies, blood disorders, diseases of the immune system, autoimmune
XX CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
XX CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
XX CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
XX CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
XX CC also useful for identifying their binding partners. The sequences shown
XX CC in AAZ86334 to AAZ86585 represent fragments of the secreted proteins
XX XX
XX SQ Sequence 415 AA;

```

```

QY 301 RRVVDVSVPLAMTGTFDLKKTLSTYIGVSKIFEESGDLTKIAPRSLKVGEAVKARLKM 360
Db 301 RRVVDVSVPLAMTGTFDLKKTLSTYIGVSKIFEESGDLTKIAPRSLKVGEAVKARLKM 360
QY 361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLIYSEKISVLFGLKIVNIGK 414
Db 361 DERGTGAGTGAQTLPMETPLVVKIDKPYLLIYSEKISVLFGLKIVNIGK 414
RESULT 7
AB053360
ID AB053360 standard; protein; 415 AA.
XX XX
XX AC AB053360;
XX XX
XX DT 06-NOV-2003 (first entry)
XX XX
XX DE Novel human secreted protein #3.
XX XX
XX KW Human; vaccine; immune system disorder; haematopoietic cell disorder;
XX KW cancer; autoimmune disorder; rheumatoid arthritis; glomerulonephritis;
XX KW HIV infection; anaemia; thrombocytopenia blood coagulation disorder;
XX KW blood platelet disorder; wound; heart attack; myocardial infarction;
XX KW stroke; scarring; asthma; graft-versus host rejection; inflammation;
XX KW hyperproliferative disorder; lymphoproliferative disorder; arrhythmia;
XX KW aberrant cellular division; cell proliferative disorder; angiodysplasia;
XX KW cardiovascular disorder; pulmonary heart disease; neovascularization;
XX KW hypertension; scar; keloid; ocular disorder; diabetic retinopathy;
XX KW uveitis; epithelial cell proliferation; neurological disease; apoptosis;
XX KW Parkinson's disease; Alzheimer's disease; Huntington's chorea; AIDS; AIDS;
XX KW amyotrophic lateral sclerosis; toxin induced liver disease; septic shock;
XX KW cachexia; anorexia; lung damage; infection.
XX XX
XX OS Homo sapiens.
XX XX
XX PN US2003065151-A1.
XX XX
XX PD 03-APR-2003.
XX XX
XX XX 04-APR-2002; 2002US-00115123.
XX PF
XX PR 16-JUN-1998; 98US-0089507P.
XX PR 16-JUN-1998; 98US-0089508P.
XX PR 16-JUN-1998; 98US-0089509P.
XX PR 16-JUN-1998; 98US-0089510P.
XX PR 22-JUN-1998; 98US-0090112P.
XX PR 22-JUN-1998; 98US-0090113P.
XX PR 15-JUN-1999; 99WO-US013418.
XX PR 14-DEC-1999; 99US-00461325.
XX XX
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Ruben SM, Ni J, Rosen CA, Wei Y, Young P, Florence K, Soppet DR;
XX PI Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R, Lafleur DW;
XX PI Olsen H, Shi Y, Moore PA, Komatsoulis G;
XX XX
XX DR WPI: 2003-531736/50.
XX DR N-PSDB; ACH66650.
XX XX
XX PT Novel antibody that binds specifically to a HCEJ069 protein, useful for
XX PT detecting the presence of a protein in a biological sample, and for
XX PT treating cancers, autoimmune disorders and HIV infection.
XX XX
XX PS Disclosure; SEQ ID NO 134; 176pp; English.
XX XX
XX CC The invention relates to an isolated antibody or its fragment that
XX CC specifically binds to a protein. The antibody is useful for detecting a
XX CC protein in a biological sample, by contacting the biological sample with
XX CC the antibody or its fragment and detecting the protein in the biological
XX CC sample. The antibody is useful for purifying, detecting and targeting the
XX CC human secreted proteins, including both in vitro and in vivo diagnostic
XX CC and therapeutic methods. The antibody is useful for immunophenotyping of

```

cell lines in biological samples and in antibody-based therapies for treating, inhibiting and preventing diseases, disorders or conditions associated with aberrant expression and/or activity of the above proteins. The antibody is useful for treating deficiencies or disorders of immune system and haematopoietic cells, for increasing differentiation and proliferation of haematopoietic cells, for treating immune deficiencies or disorders e.g. cancers, autoimmune disorders (such as rheumatoid arthritis and glomerulonephritis), HIV infection, anaemia and thrombocytopenia and as a marker for a particular immune system disease or disorder. The antibody is also useful for treating blood coagulation disorders, blood platelet disorders, wounds, heart attacks (infarction), strokes, scarring and asthma. The antibody is also useful for treating or preventing graft-versus host rejection, for modulating inflammation, for treating hyperproliferative disorders e.g. lymphoproliferative disorders and cancers, for inhibiting aberrant cellular division and for treating cell proliferative disorders. The antibody is also useful for treating cardiovascular disorders e.g. pulmonary heart disease and arrhythmia, disorders associated with neovascularization and angiogenesis, for treating hypertrophic scars and keloids, ocular disorders e.g. diabetic retinopathy and uveitis, for wound healing and disorders of epithelial cell proliferation. The antibody is also useful for treating neurological diseases e.g. Parkinson's disease, Alzheimer's disease, Huntington's chorea and amyotrophic lateral sclerosis (ALS), diseases associated with increased apoptosis e.g. AIDS, toxin induced liver disease, septic shock, cachexia and anorexia, for preventing and healing damage to lungs and for treating infectious diseases. The present sequence represents the amino acid sequence of a novel human secreted protein. Note: the sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docid=20030065151

Sequence 415 AA;

Query Match 100.0%; Score 414; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNPPTGLAIFLAVLLTVKGLKPSPPRYKALSEVQGMKMAKELARQNDLGFKLL 60
DB 1 NNPPTGLAIFLAVLLTVKGLKPSPPRYKALSEVQGMKMAKELARQNDLGFKLL 60
QY 61 KKLAFNPGRNIFLPLSLSTAFSMCLGADSTLDEIKOGFNRKMPKEDLHEGPHYII 120
DB 61 KKLAFNPGRNIFLPLSLSTAFSMCLGADSTLDEIKOGFNRKMPKEDLHEGPHYII 120
QY 121 HELTQKTODLKLSIGNTLFIIDQRLQPKRLEDAKNFYSAEITLTFNFOULEMAQKINDF 180
DB 121 HELTQKTODLKLSIGNTLFIIDQRLQPKRLEDAKNFYSAEITLTFNFOULEMAQKINDF 180
QY 121 HELTQKTODLKLSIGNTLFIIDQRLQPKRLEDAKNFYSAEITLTFNFOULEMAQKINDF 180
DB 121 HELTQKTODLKLSIGNTLFIIDQRLQPKRLEDAKNFYSAEITLTFNFOULEMAQKINDF 180
QY 181 ISQKTGKINNLINLENDPGTWMLANIYFFRARKGHEPDNVTKEEDFLEKNSVYKVP 240
DB 181 ISQKTGKINNLINLENDPGTWMLANIYFFRARKGHEPDNVTKEEDFLEKNSVYKVP 240
QY 241 MFRSGIYGVGYDKSCTILFIYQKNITAFILPBEKGLKHEKLOVDTFRMKTLLS 300
DB 241 MFRSGIYGVGYDKSCTILFIYQKNITAFILPBEKGLKHEKLOVDTFRMKTLLS 300
QY 301 RRVVDVSVRLMHTGTFDLKKTLSYIGSVKIFPEHSDLTFAIARSLKAYGEAVHKAELMK 360
DB 301 RRVVDVSVRLMHTGTFDLKKTLSYIGSVKIFPEHSDLTFAIARSLKAYGEAVHKAELMK 360
QY 361 DERGTGGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFCKIYNPIGK 414
DB 361 DERGTGGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFCKIYNPIGK 414

RESULT 8

AAW78898 standard; protein; 414 AA.

AC AAW78898;

DT 06-NOV-2001 (first entry)

XX Human protein SEQ ID NO 1560.
DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM Vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.
OS Homo sapiens.
PN WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX 20-JUN-2000; 2000US-00598075.
XX 19-JUL-2000; 2000US-00620325.
XX 01-SEP-2000; 2000US-00654936.
XX 15-SEP-2000; 2000US-00653561.
XX 20-OCT-2000; 2000US-00693325.
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSB-) HYSBQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX MPI; 2001-476283/51.
XX N-PSDB; AAK52031.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
XX
XX Claim 20; Page 3878-3879; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78823-AAW80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX

Sequence 414 AA;

Query Match 85.3%; Score 353; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNPPTGLAIFLAVLLTVKGLKPSPPRYKALSEVQGMKMAKELARQNDLGFKLL 60
DB 1 NNPPTGLAIFLAVLLTVKGLKPSPPRYKALSEVQGMKMAKELARQNDLGFKLL 60
QY 61 KKLAFNPGRNIFLPLSLSTAFSMCLGADSTLDEIKOGFNRKMPKEDLHEGPHYII 120
DB 61 KKLAFNPGRNIFLPLSLSTAFSMCLGADSTLDEIKOGFNRKMPKEDLHEGPHYII 120
QY 121 HELTQKTODLKLSIGNTLFIIDQRLQPKRLEDAKNFYSAEITLTFNFOULEMAQKINDF 180
DB 121 HELTQKTODLKLSIGNTLFIIDQRLQPKRLEDAKNFYSAEITLTFNFOULEMAQKINDF 180
QY 181 ISQKTGKINNLINLENDPGTWMLANIYFFRARKGHEPDNVTKEEDFLEKNSVYKVP 240
DB 181 ISQKTGKINNLINLENDPGTWMLANIYFFRARKGHEPDNVTKEEDFLEKNSVYKVP 240

Db 181 ISQKTHKINNLINIDPGTVMLLANYIFPRARKHEFDPNVTKBEDFLEKNSVAVPM 240
 QY MFRSGIYQVGYDDKLSCTTILEIPYQKNITAFILPDGKLGKLEKGLQVDFSRKLTLS 300
 Db 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAFILPDGKLGKLEKGLQVDFSRKLTLS 300
 QY 301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEHGDLTAKAPRSLKVGAV 353
 Db 301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEHGDLTAKAPRSLKVGAV 353
 RESULT 9
 AAU05759
 ID AAU05759 standard; protein; 358 AA.
 AC AAU05759;
 DT 24-OCT-2001 (first entry)
 DE Human NOV7 polypeptide #2.
 XX
 XX Human; NOV7; A1132990 B; fertility disorder; spermatogenesis; cardiant;
 KW cytostatic; immunomodulatory; antiproliferative; antidiabetic;
 KW cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
 KW pulmonary disorder; haematopoietic disorder; immunological disorder;
 KW inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
 KW wound healing; gene therapy.
 XX
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 311..322
 FT /label= OTHER
 FT /note= "Other= Unknown"
 XX
 XX W0200149729-A2.
 PD 12-JUL-2001.
 PD 05-JAN-2001; 2001MO-US000299.
 XX
 XX 06-JAN-2000; 2000US-0174724P.
 PR 11-JAN-2000; 2000US-0175434P.
 PR 11-JAN-2000; 2000US-0175488P.
 PR 12-JAN-2000; 2000US-0175696P.
 PR 12-JAN-2000; 2000US-0175743P.
 PR 13-JAN-2000; 2000US-0175819P.
 PR 07-AUG-2000; 2000US-0223524P.
 PR 04-JAN-2001; 2001US-00755665.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Prayaga SK, Majumder K, Tallon BF, Spaderna SK, Spytek KA,
 PI Macdougall J,
 XX
 DR WPI; 2001-418356/44.
 XX
 PT Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
 PT for treating a syndrome associated with a NOVX-associated disorder, e.g.
 PT cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
 PT pulmonary disorder.
 XX
 PS Disclosure; Page 33; 144pp; English.
 XX
 CC The invention relates to nucleic acids encoding NOVX (X being an integer
 CC from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
 CC useful in diagnosing, treating or manufacturing a medicament for a
 CC disease or disorder associated with NOVX e.g. cell proliferation (cancer
 CC and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
 CC disorders (e.g. of spermatogenesis), haematopoietic, immunological,
 CC inflammatory and tumour related disorders, emphysema, cirrhosis, wound
 CC healing. NOVX nucleic acids are also useful in gene therapy. They are
 CC also used for screening for a modulator of activity or of latency or

CC predisposition to a NOVX-associated disorder. They are also useful for
 CC determining the presence of or predisposition to a NOVX-associated
 CC disorder. The present sequence represents a version of NOV7 (A1132990 B)
 CC appearing in table 25 of the specification, which has sequence homology
 CC to an unidentified human secreted protein (HMGUS54) and to alpha anti-
 CC trypsin
 XX
 SQ Sequence 358 AA;
 XX
 Query Match 74.9%; Score 310; DB 4; Length 358;
 Best Local Similarity 100.0%; Pred. No. 4.1e-294;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 54 DLGFKLLKCLAFNPGNIFLSPISISTASMTCLGAQDSTLDEIKGFNFRKPEKDLH 113
 Db 1 DLGFKLLKCLAFNPGNIFLSPISISTASMTCLGAQDSTLDEIKGFNFRKPEKDLH 60
 QY 114 EGFHYIIHELTKQTDKLSIGNTLFDLQRLQPKFLBDKKNFYSATLLTNFQNLMA 173
 Db 61 EGFHYIIHELTKQTDKLSIGNTLFDLQRLQPKFLBDKKNFYSATLLTNFQNLMA 120
 QY 174 QKQINDPISQKTKGKINNLINIDPGTVMLLANYIFPRARKHEFDPNVTKBEDFLEKN 233
 Db 121 QKQINDPISQKTKGKINNLINIDPGTVMLLANYIFPRARKHEFDPNVTKBEDFLEKN 180
 QY 234 SSYKVPWMPFRSGIYQVGYDDKLSCTTILEIPYQKNITAFILPDGKLGKLEKGLQVTF 293
 Db 181 SSYKVPWMPFRSGIYQVGYDDKLSCTTILEIPYQKNITAFILPDGKLGKLEKGLQVTF 240
 QY 294 RMTLLSRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEHGDLTAKAPRSLKVGAV 353
 Db 241 RMTLLSRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEHGDLTAKAPRSLKVGAV 300
 QY 354 HKAELKXDER 363
 Db 301 HKAELKXDER 310
 XX
 XX
 RESULT 10
 ABB11832
 ID ABB11832 standard; peptide; 431 AA.
 XX
 AC ABB11832;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human secreted protein homologue, SEQ ID NO:2202.
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antitubercular; antidiabetic; haemostatic; antidiabetic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antitumor.
 XX
 OS Homo sapiens.
 XX
 XX W0200157188-A2.
 XX
 PN 09-AUG-2001.
 XX
 PD 05-FEB-2001; 2001MO-US003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX

PA (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX
 XX WPI: 2001-457740/49.
 DR N-PSDB; ABA09076.
 XX
 XX Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 XX Claim 20, Page 263; 1963pp; English.

CC Sequences ABA10981-ABA12330 represent 1350 novel human polypeptides, and
 CC sequence ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoietic regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX
 XX
 SQ Sequence 431 AA;

Query Match 43.7%; Score 181; DB 4; Length 431;
 Best Local Similarity 100.0%; Pred. No. 7e-168;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMPTGLAIFLAVLITVVGKLGKPSPPRYKALSEVQGMKORMAKELARQNMDDGFKLL 60
 DB 18 NMPTGLAIFLAVLITVVGKLGKPSPPRYKALSEVQGMKORMAKELARQNMDDGFKLL 77
 QY 61 KKLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKGFNFKMPEKDLHGEFHYII 120
 DB 78 KKLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKGFNFKMPEKDLHGEFHYII 137
 QY 121 HELTQKTQDLKLSIGNTLTITDQRLQQRKFLBPAKRFYSATLTLLNPNQMLEMAQKINDP 180
 DB 138 HELTQKTQDLKLSIGNTLTITDQRLQQRKFLBPAKRFYSATLTLLNPNQMLEMAQKINDP 197
 QY 181 I 181
 DB 198 I 198

RESULT 11
 AAM79882
 ID AAM79882 standard; protein; 431 AA.
 XX
 XX AAM79882;
 AC
 XX
 XX 06-NOV-2001 (first entry)
 DT
 XX
 XX Human protein SEQ ID NO 3528.
 DE

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX

OS Homo sapiens.
 XX
 XX WO200157190-A2.
 PN
 XX 09-AUG-2001.
 XX

PF 05-FEB-2001; 2001WO-US004098.
 XX

PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654935.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX

PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX

DR WPI: 2001-476283/51.
 DR N-PSDB; AAK53015.
 XX

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 PT

PS Claim 20; Page 371; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoietic regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52881), 2111
 CC (AAK52882) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX

SQ Sequence 431 AA;

Query Match 43.7%; Score 181; DB 4; Length 431;
 Best Local Similarity 100.0%; Pred. No. 7e-168;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMPTGLAIFLAVLITVVGKLGKPSPPRYKALSEVQGMKORMAKELARQNMDDGFKLL 60
 DB 18 NMPTGLAIFLAVLITVVGKLGKPSPPRYKALSEVQGMKORMAKELARQNMDDGFKLL 77
 QY 61 KKLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKGFNFKMPEKDLHGEFHYII 120

Db 78 KGLAFYNGRNIFLSPISISTAFSMLCIGAQDSTLDEIKOGFNFRKPEKDLHEGFHYII 137
 QY 121 HELTQKTQDLKLSIGNTLFIPIORLQPORKFLEDAKNFYSAETILTNPONLEMAKQINDF 180
 Db 138 HELTQKTQDLKLSIGNTLFIPIORLQPORKFLEDAKNFYSAETILTNPONLEMAKQINDF 197
 QY 181 I 181
 Db 198 I 198

RESULT 12

AAM70426
 ID AAM70426 standard; protein; 140 AA.

XX AAM70426;
 AC AAM70426;
 XX

DT 06-NOV-2001 (first entry)
 XX

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30732.
 XX

KM Human; bone marrow expressed exon; gene expression analysis; probe:
 KM microarray; cancer; leukaemia; lymphoma; myeloma.
 XX

OS Homo sapiens.
 XX

PN WO200157276-A2.
 XX

PD 09-AUG-2001.
 XX

PF 30-JAN-2001; 2001WO-US000668.
 XX

PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX

PA (MOLF-) MOLECULAR DYNAMICS INC.
 XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX

DR WPI; 2001-488900/53.
 XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX

PS Example 4; SEQ ID NO 30732; 658bp + Sequence Listing; English.
 XX

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX

SQ Sequence 140 AA;

Query Match 31.2%; Score 129; DB 4; Length 140;
 Best Local Similarity 100.0%; Pred. No. 2e-117;

Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 FSNLCIGAQDSTLDEIKOGFNFRKPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIPIQ 142
 Db 1 FSNLCIGAQDSTLDEIKOGFNFRKPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIPIQ 60

QY 143 RLQPORKFLEDAKNFYSAETILTNPONLEMAKQINDFISQKTHGKTNLLENIDPGTVM 202
 Db 61 RLQPORKFLEDAKNFYSAETILTNPONLEMAKQINDFISQKTHGKTNLLENIDPGTVM 120

QY 203 LLANYIFR 211

Db 121 LLANYIFR 129

Search completed: March 31, 2006, 10:02:29
 Job time : 224.573 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 10:02:58 ; Search time 26.0989 Seconds
(without alignments)
1526.262 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTLGAIPLAVLLTVKGL.....YSEKIPSVLFGKIVNPICK 414

Scoring matrix: BLO62
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 35
Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : PIR_80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
------------	-------------	--------	----	-------------

No matches found

Search completed: March 31, 2006, 10:08:39
Job time : 26.0989 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:55:21 ; Search time 157.105 Seconds
(without alignments)
1859.193 Million cell updates/sec

Title: US-10-664-356-1562

Perfect score: 414
Sequence: 1 MNPTGLAIFLAVLLTVKGL.....YSEKIPSVLFGKIVNPIGK 414

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 15

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database: UniProt_05.80.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	414	100.0	414 2	Q81W75 HUMAN
2	19	4.6	413 2	Q7TWF5 MOUSE
3	19	4.6	413 2	Q9CQ32 MOUSE
4	19	4.6	413 2	Q6P6M3 MOUSE
5	16	3.9	411 2	Q8R4Z1 RAT

ALIGNMENTS

RESULT 1
Q81W75 HUMAN
ID Q81W75_HUMAN PRELIMINARY; PRT; 414 AA.
AC Q81W75;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1 antitrypsin, antitrypsin), member 12 (Ol-64) (Visceral adipose-specific SERPIN)
GN Name=SERPINA12;
OS Homo sapiens (Human).
OC Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.2426038999; Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diachenko L., Maruina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinot P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.W., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RA NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RG NIH WGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
[3]
RA NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RG Chen S., Guo J.H., Yu L.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
[4]
RA NUCLEOTIDE SEQUENCE.
RC Hida K., Wada J., Zhang H.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; BC040857; AA040857.1; -; mRNA.
DR EMBL; AY177692; AA018649.1; -; mRNA.
DR HSSP; P01009; 10MB.
DR Ensembl; ENSG00000165953; Homo sapiens.
DR HGNC; HGNC:18359; SERPINA12.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin, 1.
DR SMART; SM00093; SERPIN, 1.
KW Serpin.
SQ SEQUENCE 414 AA; 47175 MW; 5C70F1AB5935661C CRC64;
Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPTGLAIFLAVLLTVKGLKSPSPRYKALSEVQGTQRMVAKELARQNDLGFRL 60
DB 1 MNPTGLAIFLAVLLTVKGLKSPSPRYKALSEVQGTQRMVAKELARQNDLGFRL 60
QY 61 KKLAFVNGRNIFLSPISSTAFSMLCTGAQDSTLDSIKGFNRKMKPEQDLSGPHYII 120
DB 61 KKLAFVNGRNIFLSPISSTAFSMLCTGAQDSTLDSIKGFNRKMKPEQDLSGPHYII 120
QY 121 HELTQKTDKLKLSIGNTLFTDRLQPKRFLBDAKNFSAETILTNQNLMAQKQINDF 180
DB 121 HELTQKTDKLKLSIGNTLFTDRLQPKRFLBDAKNFSAETILTNQNLMAQKQINDF 180
QY 181 ISQKTHGKINMLIENIDPGVTMLLANYIFPRARKHEFDNVTKEDPFLKNSVAVPM 240
DB 181 ISQKTHGKINMLIENIDPGVTMLLANYIFPRARKHEFDNVTKEDPFLKNSVAVPM 240
QY 241 MPRSGIYGVGDKLSTCTIEIPYOKNITAFILPBGKDKHEKGIQVTPSRMKTLLS 300
DB 241 MPRSGIYGVGDKLSTCTIEIPYOKNITAFILPBGKDKHEKGIQVTPSRMKTLLS 300
QY 301 RRVVDVSVPLHNTGTFDLKLTSLYIGVSKIFPEHGDLTKIAPHSRLKGAAYHAKELKM 360

Dd	301	RRVADVSPRLMTGTGTFDLKKTLSYIGSVSKPIEHBGDLTKIAPHRSIKVGEAVHKAELKM
Cy	361	DERGREGAAGTCGAQTLPMETPLVVKIDRKYLLIIYSSEKIPSTLFLCKIYNPBGK 414
Dd	361	DERGREGAAGTGAQTLPMETPLVVRIDKPYLLLIYSEKIPSYLFLGKIYNPIGK 414

RESULT 2
O7TMP5_MOUSE PRELIMINARY; PRT; 413 AA.

ID	O7TMP5_MOUSE	PRT;	413 AA.
AC	O7TMP5:		
DT	01-OCT-2003 (TREMBLrel. 25, Created)		
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Visceral adipose-specific SERPIN.		
GN	Name=SerpinA12;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Swiss Webster.		
RL	Hida K., Wada J., Zhang H.,		
CC	Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.		
-1	SIMILARITY: Belongs to the serpin family.		
DR	EMBL; AY326419; AAP88383.1; -; mRNA.		
DR	HSSP; P01008; IATH.		
DR	MGI; MGI:1915304; SerpinA12.		
DR	GO; GO:0005615; Extracellular space; TAS.		
DR	InterPro; IPR000295; Prot_inh_serp2.		
DR	InterPro; IPR000215; Prot_inh_serpin.		
DR	Pfam; PF00079; Serpin_1.		
DR	PRINTS; PR00780; LEUSERPINIT.		
DR	SMART; SMO0093; SERPIN.1.		
DR	PROSITE; PS00284; SERPIN; 1.		
KW	Serpin.		
SQ	SEQUENCE 413 AA; 47674 MW; EE2B3B08C2DD418F CRC64;		

Query Match 4.6%; Score 19; DB 2; Length 413;
Best Local Similarity 100.0%; Pred.No. 4-5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Cy	344	HRSLKVGSAVHKAEIKMDE 362
Dd	344	HRSLKVGSAVHKAEIKMDE 362

RESULT 3
O9CQ32_MOUSE PRELIMINARY; PRT; 413 AA.

ID	O9CQ32_MOUSE	PRT;	413 AA.
AC	O9CQ32:		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-FEB-2005 (TREMBLrel. 29, Last annotation update)		
DE	Mus musculus o day neonate skin cDNA. RIKEN full-length enriched library, clone:4632419U12 product:hypothetical Serpins containing protein, full insert sequence (Mus musculus 17 days embryo head cDNA,		
DE	RIKEN full-length enriched library, clone:3300001F13		
DE	product:hypothetical Serpins containing protein, full insert sequence).		
GN	Name=SerpinA12;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Head, and Skin;		
RC	MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;		
RA	Carninci P., Hayashizaki Y.;		

RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).

[2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX MEDLINE=1086560; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai Y., Shimagawa A., Shibata K., Yoshino M., Itoh M.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi T.,
RA Saito K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Sakai K., Okazaki Y., Gojobori T., Bono H., Kauckawa T., Sato R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirral L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baren G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein J.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guetlichin S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehama Y., Mazzarelli U., Mombaerres P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyokawa K., Wang K.H., Wetz C., Whitaker C., Winking L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

[3]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX MEDLINE=22354683; PubMed=12466551; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirral L.M., Carninci A., Matsuda H., Batalov S., Betzel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough U.,
RA Gimond S., Guetlichin S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G.,
RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramchandran S.,
RA Ravasi T., Reed U.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sanderlin A., Schneider C., Sempke C.A., Setton M., Shimada K.,
RA Sultana R., Takenda Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Winking L.G., Wyszynski-Boris A., Yangisawa M., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirotsune-Kishikawa T., Konno H., Nakamura M., Sakazune N., Sato K.,
RA Shiraoki T., Waki K., Kawai J., Aitawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kigawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shimagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).

[4]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX MEDLINE=20499317; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
RA Kamei K., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1517-1630(2000).

[5]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aitawa K., Nagaoaka S., Sasaki N., Carninci P.,

RA Komno H., Akiyama J., Nishi K., Kitsuai T., Teshiro H., Itoh M.,
RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed sequencing.",
RL Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukutani S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Komno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; AK014589; BAB29447.1; -; mRNA.
DR EMBL; AK014346; BAB29287.1; -; mRNA.
DR HSSP; P01008; IATH.
DR Ensembl; ENSMUSG00000041567; Mus musculus.
DR MGI; MGI:1915304; Serpina12.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000295; Prot_inh_Leerp2.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR PRINTS; PR00780; LEUSERPINII.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR Hypothetical protein; Serpin.
SQ SEQUENCE 413 AA; 47634 MW; DOAB8E1BE24FD60A CRC64;
Query Match 4.6%; Score 19; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 344 HRSIKVGEAVHAKELKXDE 362
DB 344 HRSIKVGEAVHAKELKXDE 362
RESULT 4
Q6PEM3_MOUSE PRELIMINARY; PRT; 413 AA.
AC 06PEM3_MOUSE PRELIMINARY; PRT; 413 AA.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Visceral adipose-specific SERPIN.
GN Name=Serpina12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Jaw and Limb;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Dergs J.G.,
RA Klausner R.D., Collins P.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatkovich L., Marulanda K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Rata S.A., McGraw P.J., McKernan K.J., Malek J.A., Gunatarte P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywiński M.I., Skalska U., Smalins D.E.,
RA Scherich A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Jaw and Limb;
RG NIH MGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; BC062143; AAH62143.1; -; mRNA.
DR HSSP; P01008; IATH.
DR Ensembl; ENSMUSG00000041567; Mus musculus.
DR MGI; MGI:1915304; Serpina12.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000295; Prot_inh_Leerp2.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR PRINTS; PR00780; LEUSERPINII.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
DR Serpin.
SQ SEQUENCE 413 AA; 47630 MW; CE1940BA2EBE5811 CRC64;
Query Match 4.6%; Score 19; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 344 HRSIKVGEAVHAKELKXDE 362
DB 344 HRSIKVGEAVHAKELKXDE 362
RESULT 5
Q6RAZ1_RAT PRELIMINARY; PRT; 411 AA.
AC 06RAZ1_RAT PRELIMINARY; PRT; 411 AA.
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 24, Last annotation update)
DE Visceral adipose tissue specific SERPIN.
GN Name=Serpina12; Synonym=Vaspin;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OLETF; TISSUE=Visceral adipose;
RA Hida K., Wada J., Zhang H., Shikata K., Makino H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; AF245398; ALJ9574.1; -; mRNA.
DR HSSP; P01008; IATH.
DR Ensembl; ENSRNOG00000009710; Rattus norvegicus.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000295; Prot_inh_Leerp2.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR PRINTS; PR00780; LEUSERPINII.
DR SMART; SM00093; SERPIN; 1.

KW Serpin. 411 AA; 47527 MW; 29FA271FF8CC8A2D CRC64;
SQ SEQUENCE

Query Match 3.9%; Score 16; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 NIFLSPUSISTAFSML 86
|||
Db 71 NIFLSPUSISTAFSML 86

Search completed: March 31, 2006, 10:07:43
Job time : 159.105 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: March 31, 2006, 10:08:07 ; Search time 33.775 Seconds
(without alignments)
1013.403 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTGLAIFLAVALTVKGLP.....YSEKIPSVLFGKIVNPIGK 414

Scoring table: **ORF60**
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size: **35**

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	414	100.0	414	2	US-09-755-665-14
2	414	100.0	414	2	US-09-755-665-55
3	414	100.0	414	2	US-09-755-665-56
4	414	100.0	415	2	US-09-461-325-134
5	414	100.0	415	2	US-10-012-542-134
6	414	100.0	415	2	US-10-115-123-134
7	310	74.9	361	2	US-09-755-665-57

ALIGNMENTS

RESULT 1
US-09-755-665-14
; Sequence 14, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailion, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14

; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-14

Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNPTGLAIFLAVALTVKGLKPSFRNKALSEVGMQRMAKELARONMDLGRKL	60
DB	1	MNPTGLAIFLAVALTVKGLKPSFRNKALSEVGMQRMAKELARONMDLGRKL	60
QY	61	KCLAFVNGRNIFLPSLSTAFSMLCLGADSTLDEIKGFNFRKPEKDLHEGFYII	120
DB	61	KCLAFVNGRNIFLPSLSTAFSMLCLGADSTLDEIKGFNFRKPEKDLHEGFYII	120
QY	121	HELTOKTQDLKLSIGNTLFDORLQPKRFLDPAKNFYSAFTITNFQNLMAQKQINDF	180
DB	121	HELTOKTQDLKLSIGNTLFDORLQPKRFLDPAKNFYSAFTITNFQNLMAQKQINDF	180
QY	181	ISOKTGKINNLLENTIDPGTMLLANYIFRARKHEFDNNTKEEDFLEKSSVAVPM	240
DB	181	ISOKTGKINNLLENTIDPGTMLLANYIFRARKHEFDNNTKEEDFLEKSSVAVPM	240
QY	241	MFSSGIYQVGYDDKLSCTTIEIPYQKNITAIFFLPDEKGLKHEKGLQVTFPSRWKTLIS	300
DB	241	MFSSGIYQVGYDDKLSCTTIEIPYQKNITAIFFLPDEKGLKHEKGLQVTFPSRWKTLIS	300
QY	301	RRVVDVSPRLHNTGTFPDLKKTLSYIGVSKIPEEHGDLTKIAPRSLKVGSAVHKAELKM	360
DB	301	RRVVDVSPRLHNTGTFPDLKKTLSYIGVSKIPEEHGDLTKIAPRSLKVGSAVHKAELKM	360
QY	361	DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFGKIVNPIGK	414
DB	361	DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFGKIVNPIGK	414

RESULT 2
US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailion, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-55

Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNPTGLAIFLAVALTVKGLKPSFRNKALSEVGMQRMAKELARONMDLGRKL 60

```
Db 1 MNPITGLAIFLAVLLTVVGLKLPSPSPNNYKALSEVQGMKORMAAKELARQNMDDGFKLL 60
Qy 61 KKLAFYNGRNIFLSPILSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHSGFHYII 120
Db 61 KKLAFYNGRNIFLSPILSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHSGFHYII 120
Qy 121 HELTQKTDKLKLSIGNTLFIIDQRLQPKFLEDAKNFYSAETILLNPNQLEMAQKQINDF 180
Db 121 HELTQKTDKLKLSIGNTLFIIDQRLQPKFLEDAKNFYSAETILLNPNQLEMAQKQINDF 180
Qy 181 ISQKTHGKINNLIENIDPGTWMLANYIFPRARWGHFDPNVTKEEDFLEKNSSVKVP 240
Db 181 ISQKTHGKINNLIENIDPGTWMLANYIFPRARWGHFDPNVTKEEDFLEKNSSVKVP 240
Qy 241 MFRSGIYGVYDDKLSCTILIEIPYQKNITAFILPDEGKLKHLKGLQVDTFSRMKTLIS 300
Db 241 MFRSGIYGVYDDKLSCTILIEIPYQKNITAFILPDEGKLKHLKGLQVDTFSRMKTLIS 300
Qy 301 RRVVDVSVRLHMTGTFDLKLTSLYIGVSKIPEHGDLTAKIAPHSLKVGAEVHKAELKM 360
Db 301 RRVVDVSVRLHMTGTFDLKLTSLYIGVSKIPEHGDLTAKIAPHSLKVGAEVHKAELKM 360
Qy 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
Db 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
```

RESULT 3

```
US-09-755-665-56
; Sequence 36, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-56
```

```
Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MNPITGLAIFLAVLLTVVGLKLPSPSPNNYKALSEVQGMKORMAAKELARQNMDDGFKLL 60
Db 1 MNPITGLAIFLAVLLTVVGLKLPSPSPNNYKALSEVQGMKORMAAKELARQNMDDGFKLL 60
Qy 61 KKLAFYNGRNIFLSPILSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHSGFHYII 120
Db 61 KKLAFYNGRNIFLSPILSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHSGFHYII 120
Qy 121 HELTQKTDKLKLSIGNTLFIIDQRLQPKFLEDAKNFYSAETILLNPNQLEMAQKQINDF 180
Db 121 HELTQKTDKLKLSIGNTLFIIDQRLQPKFLEDAKNFYSAETILLNPNQLEMAQKQINDF 180
Qy 181 ISQKTHGKINNLIENIDPGTWMLANYIFPRARWGHFDPNVTKEEDFLEKNSSVKVP 240
Db 181 ISQKTHGKINNLIENIDPGTWMLANYIFPRARWGHFDPNVTKEEDFLEKNSSVKVP 240
```

```
Qy 241 MFRSGIYGVYDDKLSCTILIEIPYQKNITAFILPDEGKLKHLKGLQVDTFSRMKTLIS 300
Db 241 MFRSGIYGVYDDKLSCTILIEIPYQKNITAFILPDEGKLKHLKGLQVDTFSRMKTLIS 300
Qy 301 RRVVDVSVRLHMTGTFDLKLTSLYIGVSKIPEHGDLTAKIAPHSLKVGAEVHKAELKM 360
Db 301 RRVVDVSVRLHMTGTFDLKLTSLYIGVSKIPEHGDLTAKIAPHSLKVGAEVHKAELKM 360
Qy 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
Db 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
```

RESULT 4

```
US-09-461-325-134
; Sequence 134, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-461-325-134
```

```
Query Match 100.0%; Score 414; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MNPITGLAIFLAVLLTVVGLKLPSPSPNNYKALSEVQGMKORMAAKELARQNMDDGFKLL 60
Db 1 MNPITGLAIFLAVLLTVVGLKLPSPSPNNYKALSEVQGMKORMAAKELARQNMDDGFKLL 60
Qy 61 KKLAFYNGRNIFLSPILSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHSGFHYII 120
Db 61 KKLAFYNGRNIFLSPILSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHSGFHYII 120
Qy 121 HELTQKTDKLKLSIGNTLFIIDQRLQPKFLEDAKNFYSAETILLNPNQLEMAQKQINDF 180
Db 121 HELTQKTDKLKLSIGNTLFIIDQRLQPKFLEDAKNFYSAETILLNPNQLEMAQKQINDF 180
Qy 181 ISQKTHGKINNLIENIDPGTWMLANYIFPRARWGHFDPNVTKEEDFLEKNSSVKVP 240
Db 181 ISQKTHGKINNLIENIDPGTWMLANYIFPRARWGHFDPNVTKEEDFLEKNSSVKVP 240
Qy 241 MFRSGIYGVYDDKLSCTILIEIPYQKNITAFILPDEGKLKHLKGLQVDTFSRMKTLIS 300
Db 241 MFRSGIYGVYDDKLSCTILIEIPYQKNITAFILPDEGKLKHLKGLQVDTFSRMKTLIS 300
```

Qy 301 RRVVDVSVPLHMTGTEDLTKKTLISYIGVSKIPEEHGDLTKIAPHRSILKVGSAVHKAELKM 360
Db 301 RRVVDVSVPLHMTGTEDLTKKTLISYIGVSKIPEEHGDLTKIAPHRSILKVGSAVHKAELKM 360
Qy 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIKIVNPIGK 414
Db 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIKIVNPIGK 414

RESULT 5

US-10-012-542-134
; Sequence 134, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-012-542-134

Query Match 100.0%; Score 414; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPTGLAIFLAVALTVYKGLIKPSFSPRNYKALSEVGWQRMMAKELARQNDLGFRL 60
Db 1 MNPTGLAIFLAVALTVYKGLIKPSFSPRNYKALSEVGWQRMMAKELARQNDLGFRL 60
Qy 61 KKAIFYNPGNNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMBEKDLHGFHYII 120
Db 61 KKAIFYNPGNNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMBEKDLHGFHYII 120
Qy 121 HELTQKTQDCLKSIGNTLFLDQRLQPKRFLBDKKNFYSAETIITNFQNLMAQKQINDF 180
Db 121 HELTQKTQDCLKSIGNTLFLDQRLQPKRFLBDKKNFYSAETIITNFQNLMAQKQINDF 180
Qy 121 ISQTHGKINNLIENIDPGTVMLLANYIFPRARKHEFDPNVTKBEDFLEKNSSVVPM 240
Db 121 ISQTHGKINNLIENIDPGTVMLLANYIFPRARKHEFDPNVTKBEDFLEKNSSVVPM 240
Qy 181 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKLKHEKGLQVDTFSWKTLIS 300
Db 181 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKLKHEKGLQVDTFSWKTLIS 300
Qy 241 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKLKHEKGLQVDTFSWKTLIS 300
Db 241 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKLKHEKGLQVDTFSWKTLIS 300
Qy 301 RRVVDVSVPLHMTGTEDLTKKTLISYIGVSKIPEEHGDLTKIAPHRSILKVGSAVHKAELKM 360
Db 301 RRVVDVSVPLHMTGTEDLTKKTLISYIGVSKIPEEHGDLTKIAPHRSILKVGSAVHKAELKM 360

Qy 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIKIVNPIGK 414
Db 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIKIVNPIGK 414

RESULT 6

US-10-115-123-134
; Sequence 134, Application US/10115123
; Patent No. 674216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P202930APD2
; CURRENT APPLICATION NUMBER: US/10/115,123
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-115-123-134

Query Match 100.0%; Score 414; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPTGLAIFLAVALTVYKGLIKPSFSPRNYKALSEVGWQRMMAKELARQNDLGFRL 60
Db 1 MNPTGLAIFLAVALTVYKGLIKPSFSPRNYKALSEVGWQRMMAKELARQNDLGFRL 60
Qy 61 KKAIFYNPGNNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMBEKDLHGFHYII 120
Db 61 KKAIFYNPGNNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMBEKDLHGFHYII 120
Qy 121 HELTQKTQDCLKSIGNTLFLDQRLQPKRFLBDKKNFYSAETIITNFQNLMAQKQINDF 180
Db 121 HELTQKTQDCLKSIGNTLFLDQRLQPKRFLBDKKNFYSAETIITNFQNLMAQKQINDF 180
Qy 121 ISQTHGKINNLIENIDPGTVMLLANYIFPRARKHEFDPNVTKBEDFLEKNSSVVPM 240
Db 121 ISQTHGKINNLIENIDPGTVMLLANYIFPRARKHEFDPNVTKBEDFLEKNSSVVPM 240
Qy 181 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKLKHEKGLQVDTFSWKTLIS 300
Db 181 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKLKHEKGLQVDTFSWKTLIS 300
Qy 241 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKLKHEKGLQVDTFSWKTLIS 300
Db 241 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKLKHEKGLQVDTFSWKTLIS 300
Qy 301 RRVVDVSVPLHMTGTEDLTKKTLISYIGVSKIPEEHGDLTKIAPHRSILKVGSAVHKAELKM 360
Db 301 RRVVDVSVPLHMTGTEDLTKKTLISYIGVSKIPEEHGDLTKIAPHRSILKVGSAVHKAELKM 360
Qy 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIKIVNPIGK 414
Db 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIKIVNPIGK 414

RESULT 7
US-09-755-665-57
Sequence 57, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tailon, Bruce B.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 361
TYPR: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(361)
OTHER INFORMATION: wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
US-09-755-665-57

Send dates

Query Match 74.9%; Score 310; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 2.3e-292;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 DLGFKLLKLAAPNPGNIFLPLSLSTAFSLCLGAQDSTLDEIKGFNFRMPKDLH 113
DB 1 DLGFKLLKLAAPNPGNIFLPLSLSTAFSLCLGAQDSTLDEIKGFNFRMPKDLH 60
QY 114 EGFHYIHELTOTODLKLSIGNTLFIIDRLQPKPKLEDAKNFYSATILTNFONLEMA 173
DB 61 EGFHYIHELTOTODLKLSIGNTLFIIDRLQPKPKLEDAKNFYSATILTNFONLEMA 120
QY 174 OKQINDFISQKTHGKINNLINENIDPGTMLANYIFPRAMKGFDPNVTKEEDFFLEKN 233
DB 121 OKQINDFISQKTHGKINNLINENIDPGTMLANYIFPRAMKGFDPNVTKEEDFFLEKN 180
QY 234 SSVKVPMMFRSGIYQVGYDDKLSCTTLEIPYQKNTAIFLDPDEGKLKHEKGLQVDTFS 293
DB 181 SSVKVPMMFRSGIYQVGYDDKLSCTTLEIPYQKNTAIFLDPDEGKLKHEKGLQVDTFS 240
QY 294 RMKTLISRRVVDVSFRLHMTGFEDLKKTLSTYGVSKIPREHGLTKIAPHRSIAKVGAV 353
DB 241 RMKTLISRRVVDVSFRLHMTGFEDLKKTLSTYGVSKIPREHGLTKIAPHRSIAKVGAV 300
QY 354 HKAEIKMDER 363
DB 301 HKAEIKMDER 310

Search completed: March 31, 2006, 10:09:51
Job time : 33.775 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 10:08:54 ; Search time 120.26 Seconds
(without alignments)
1438.400 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTLGAIPLAVLITVKGSL.....YSEKIPSVLFGKIVNPICK 414

* Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size: 15

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database: Published Applications AA Main:
1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	414	100.0	414	3	US-09-755-665-14
2	414	100.0	414	3	US-09-755-665-55
3	414	100.0	414	3	US-09-755-665-56
4	414	100.0	414	4	US-10-168-425-12
5	414	100.0	414	4	US-10-629-248-14
6	414	100.0	414	4	US-10-629-248-55
7	414	100.0	414	4	US-10-629-248-56
8	414	100.0	414	4	US-10-012-542-134
9	414	100.0	414	4	US-10-115-123-134
10	414	100.0	414	4	US-10-800-834-134
11	310	74.9	361	3	US-09-755-665-57
12	310	74.9	361	4	US-10-629-248-57
13	181	43.7	431	4	US-10-276-774-2202
14	129	31.2	140	3	US-09-864-761-48438

ALIGNMENTS

RESULT 1
US-09-755-665-14 Application US/09755665
; Sequence 14, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.

APPLICANT: Spaderna, Steven K.
APPLICANT: Spyttek, Kimberly A.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-14

Query Match 100.0%; Score 414; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNPTLGAIPLAVLITVKGSLKPSFSPRNKALSEVQGMQMAKELARQNDLGFKL	60
DB	1	MNPTLGAIPLAVLITVKGSLKPSFSPRNKALSEVQGMQMAKELARQNDLGFKL	60
QY	61	KGLAFVNGRNTFSPISSTAFSMLCIGAQDSTLDEIKQGFNRKMKPEKDLHGPHYII	120
DB	61	KGLAFVNGRNTFSPISSTAFSMLCIGAQDSTLDEIKQGFNRKMKPEKDLHGPHYII	120
QY	121	HELTQKTDKLKLSIGNTLFDQRLQPKFLEDAKNFSAETLLTNFQNLMAQKQINDF	180
DB	121	HELTQKTDKLKLSIGNTLFDQRLQPKFLEDAKNFSAETLLTNFQNLMAQKQINDF	180
QY	181	ISQTHGKINLLENIDPGTWMLLANYIFPRARKHEFDNVTKEEDFLEKSSVQVPM	240
DB	181	ISQTHGKINLLENIDPGTWMLLANYIFPRARKHEFDNVTKEEDFLEKSSVQVPM	240
QY	241	MPSGTYQVGYDRLKSTLIEIPQKNITAFILPBGKIKHLKGLQVTFPSWKTLIS	300
DB	241	MPSGTYQVGYDRLKSTLIEIPQKNITAFILPBGKIKHLKGLQVTFPSWKTLIS	300
QY	301	RRVVDVSPRLAMTGTFDLKKTLISYIGSVKIFPEHGDLTICLAPRSLKVGSAVHKELKM	360
DB	301	RRVVDVSPRLAMTGTFDLKKTLISYIGSVKIFPEHGDLTICLAPRSLKVGSAVHKELKM	360
QY	361	DERGTGAGTGAQTLPMTETPLVVKIDKPYLLIYSEKIPSVFLGKIVNPICK	414
DB	361	DERGTGAGTGAQTLPMTETPLVVKIDKPYLLIYSEKIPSVFLGKIVNPICK	414

RESULT 2
US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spyttek, Kimberly A.
; APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens

US-09-755-665-55

Query Match 100.0%; Score 414; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLLTVYKGLKPSFSPRNKALSEVQGMKORMAKELARQNDLGFKLL 60
DB 1 MNPTGLAIFLAVLLTVYKGLKPSFSPRNKALSEVQGMKORMAKELARQNDLGFKLL 60
QY 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
DB 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
QY 121 HELTQKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180
DB 121 HELTQKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180
QY 181 ISQKTHGKINNLIENIDPGTVMILANYIFPRARKHEDPNVTKEEDFLEKNSSVKVP 240
DB 181 ISQKTHGKINNLIENIDPGTVMILANYIFPRARKHEDPNVTKEEDFLEKNSSVKVP 240
QY 241 MFRSGIYQVGYDDKLSCTTILFIYQKNITAI FILPDEGKLNLEKGLQVDTFSRWKTLIS 300
DB 241 MFRSGIYQVGYDDKLSCTTILFIYQKNITAI FILPDEGKLNLEKGLQVDTFSRWKTLIS 300
QY 301 RRVVDVSVPLAHNTGTFDLKKTLSYIGVSKI FEEHGDLTIAFHSLSKVGSAVHAKELKM 360
DB 301 RRVVDVSVPLAHNTGTFDLKKTLSYIGVSKI FEEHGDLTIAFHSLSKVGSAVHAKELKM 360
QY 361 DERGTGAAGTGAGTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIVNPICK 414
DB 361 DERGTGAAGTGAGTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIVNPICK 414

RESULT 3

US-09-755-665-56
Sequence 56; Application US/09755665
Patent No. US20020107186A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce E.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-56

Query Match 100.0%; Score 414; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLLTVYKGLKPSFSPRNKALSEVQGMKORMAKELARQNDLGFKLL 60
DB 1 MNPTGLAIFLAVLLTVYKGLKPSFSPRNKALSEVQGMKORMAKELARQNDLGFKLL 60
QY 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
DB 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
QY 121 HELTQKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180
DB 121 HELTQKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180

DB 121 HELTQKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180
QY 181 ISQKTHGKINNLIENIDPGTVMILANYIFPRARKHEDPNVTKEEDFLEKNSSVKVP 240
DB 181 ISQKTHGKINNLIENIDPGTVMILANYIFPRARKHEDPNVTKEEDFLEKNSSVKVP 240
QY 241 MFRSGIYQVGYDDKLSCTTILFIYQKNITAI FILPDEGKLNLEKGLQVDTFSRWKTLIS 300
DB 241 MFRSGIYQVGYDDKLSCTTILFIYQKNITAI FILPDEGKLNLEKGLQVDTFSRWKTLIS 300
QY 301 RRVVDVSVPLAHNTGTFDLKKTLSYIGVSKI FEEHGDLTIAFHSLSKVGSAVHAKELKM 360
DB 301 RRVVDVSVPLAHNTGTFDLKKTLSYIGVSKI FEEHGDLTIAFHSLSKVGSAVHAKELKM 360
QY 361 DERGTGAAGTGAGTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIVNPICK 414
DB 361 DERGTGAAGTGAGTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIVNPICK 414

RESULT 4

US-10-168-425-12
Sequence 12; Application US/10168425
Publication No. US20030124706A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YANG, Junming
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BURFORD, Neil
APPLICANT: HU-YOUNG, Janice
APPLICANT: LU, Dying Aina M.
APPLICANT: REDDY, Roopa
APPLICANT: NGUYEN, Damien B.
APPLICANT: TANG, Y. Tom
APPLICANT: YAO, Monique G.
APPLICANT: TAL, Preeti
TITLE OF INVENTION: PROTEASES
FILE REFERENCE: PI-0003 PCT
CURRENT APPLICATION NUMBER: US/10/168,425
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903
PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO 12
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030124706A1 7257324CD1
US-10-168-425-12

Query Match 100.0%; Score 414; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLLTVYKGLKPSFSPRNKALSEVQGMKORMAKELARQNDLGFKLL 60
DB 1 MNPTGLAIFLAVLLTVYKGLKPSFSPRNKALSEVQGMKORMAKELARQNDLGFKLL 60
QY 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
DB 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
QY 121 HELTQKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180
DB 121 HELTQKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180
QY 181 ISQKTHGKINNLIENIDPGTVMILANYIFPRARKHEDPNVTKEEDFLEKNSSVKVP 240
DB 181 ISQKTHGKINNLIENIDPGTVMILANYIFPRARKHEDPNVTKEEDFLEKNSSVKVP 240

QY 241 MFRSGIYGVGDDKLSCTIIEIPYQKNITAFILPDEGKLNLEKGLQVDFSRWKTLLS 300
DB 241 MFRSGIYGVGDDKLSCTIIEIPYQKNITAFILPDEGKLNLEKGLQVDFSRWKTLLS 300
QY 301 RRVVDSVPRILMTGTFDLKKTLISYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
DB 301 RRVVDSVPRILMTGTFDLKKTLISYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
QY 361 DERGTGAAGTGAOTLPMTPLVVKIDKPYLLIYSEKIPSVLFGKIIVNPIGK 414
DB 361 DERGTGAAGTGAOTLPMTPLVVKIDKPYLLIYSEKIPSVLFGKIIVNPIGK 414

RESULT 5

US-10-629-248-14
; Sequence 14, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tallon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/10/629,248
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-629-248-14

Query Match 100.0%; Score 414; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTLGLAIFLAVALITVKGILKSPSPRNRYKALSEVQGMKORMAKELARQNDLGFRL 60
DB 1 MNPTLGLAIFLAVALITVKGILKSPSPRNRYKALSEVQGMKORMAKELARQNDLGFRL 60
QY 61 KCLAFYVPGNNIFLSPISISTAFPSMLCIGAODSTLDEIKGFNFRKQPEKDLHGPHYII 120
DB 61 KCLAFYVPGNNIFLSPISISTAFPSMLCIGAODSTLDEIKGFNFRKQPEKDLHGPHYII 120
QY 121 HELTQTKDQLKLSIGNTLFIIDRLQPRKFLDANKFYSAETIITNFONLEMAQKQINDF 180
DB 121 HELTQTKDQLKLSIGNTLFIIDRLQPRKFLDANKFYSAETIITNFONLEMAQKQINDF 180
QY 121 HELTQTKDQLKLSIGNTLFIIDRLQPRKFLDANKFYSAETIITNFONLEMAQKQINDF 180
DB 121 HELTQTKDQLKLSIGNTLFIIDRLQPRKFLDANKFYSAETIITNFONLEMAQKQINDF 180
QY 181 ISOETHKKNLLENIDPGVTMLANYIPFRAKWKHEPDVNTYEBDFLEKNSVVKPM 240
DB 181 ISOETHKKNLLENIDPGVTMLANYIPFRAKWKHEPDVNTYEBDFLEKNSVVKPM 240
QY 181 ISOETHKKNLLENIDPGVTMLANYIPFRAKWKHEPDVNTYEBDFLEKNSVVKPM 240
DB 181 ISOETHKKNLLENIDPGVTMLANYIPFRAKWKHEPDVNTYEBDFLEKNSVVKPM 240
QY 241 MFRSGIYGVGDDKLSCTIIEIPYQKNITAFILPDEGKLNLEKGLQVDFSRWKTLLS 300
DB 241 MFRSGIYGVGDDKLSCTIIEIPYQKNITAFILPDEGKLNLEKGLQVDFSRWKTLLS 300
QY 301 RRVVDSVPRILMTGTFDLKKTLISYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
DB 301 RRVVDSVPRILMTGTFDLKKTLISYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
QY 361 DERGTGAAGTGAOTLPMTPLVVKIDKPYLLIYSEKIPSVLFGKIIVNPIGK 414
DB 361 DERGTGAAGTGAOTLPMTPLVVKIDKPYLLIYSEKIPSVLFGKIIVNPIGK 414

RESULT 6

US-10-629-248-55
; Sequence 55, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tallon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/10/629,248
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-629-248-55

Query Match 100.0%; Score 414; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTLGLAIFLAVALITVKGILKSPSPRNRYKALSEVQGMKORMAKELARQNDLGFRL 60
DB 1 MNPTLGLAIFLAVALITVKGILKSPSPRNRYKALSEVQGMKORMAKELARQNDLGFRL 60
QY 61 KCLAFYVPGNNIFLSPISISTAFPSMLCIGAODSTLDEIKGFNFRKQPEKDLHGPHYII 120
DB 61 KCLAFYVPGNNIFLSPISISTAFPSMLCIGAODSTLDEIKGFNFRKQPEKDLHGPHYII 120
QY 121 HELTQTKDQLKLSIGNTLFIIDRLQPRKFLDANKFYSAETIITNFONLEMAQKQINDF 180
DB 121 HELTQTKDQLKLSIGNTLFIIDRLQPRKFLDANKFYSAETIITNFONLEMAQKQINDF 180
QY 121 HELTQTKDQLKLSIGNTLFIIDRLQPRKFLDANKFYSAETIITNFONLEMAQKQINDF 180
DB 121 HELTQTKDQLKLSIGNTLFIIDRLQPRKFLDANKFYSAETIITNFONLEMAQKQINDF 180
QY 181 ISOETHKKNLLENIDPGVTMLANYIPFRAKWKHEPDVNTYEBDFLEKNSVVKPM 240
DB 181 ISOETHKKNLLENIDPGVTMLANYIPFRAKWKHEPDVNTYEBDFLEKNSVVKPM 240
QY 241 MFRSGIYGVGDDKLSCTIIEIPYQKNITAFILPDEGKLNLEKGLQVDFSRWKTLLS 300
DB 241 MFRSGIYGVGDDKLSCTIIEIPYQKNITAFILPDEGKLNLEKGLQVDFSRWKTLLS 300
QY 301 RRVVDSVPRILMTGTFDLKKTLISYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
DB 301 RRVVDSVPRILMTGTFDLKKTLISYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
QY 361 DERGTGAAGTGAOTLPMTPLVVKIDKPYLLIYSEKIPSVLFGKIIVNPIGK 414
DB 361 DERGTGAAGTGAOTLPMTPLVVKIDKPYLLIYSEKIPSVLFGKIIVNPIGK 414

RESULT 7

US-10-629-248-56
; Sequence 56, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tallon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

```
/ FILE REFERENCE: 15966-631
/ CURRENT APPLICATION NUMBER: US/10/629,248
/ CURRENT FILING DATE: 2003-07-28
/ PRIOR APPLICATION NUMBER: US/09/755,665
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
/ PRIOR FILING DATE: 2000-01-06
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 56
/ LENGTH: 414
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-10-629-248-56

Query Match      100.0%; Score 414; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPFLGLAIFLAVLLTVKGLIKPSFSPRNYKALSEVQGWKORMAAKELARQNMNDLGFKLL 60
DB 1 MNPFLGLAIFLAVLLTVKGLIKPSFSPRNYKALSEVQGWKORMAAKELARQNMNDLGFKLL 60
QY 61 KKLAFNPGNITFLSPLSISTAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHSGFYII 120
DB 61 KKLAFNPGNITFLSPLSISTAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHSGFYII 120
QY 121 HELTQKTQDLKLSIGNTLFIQRLQPKRFLBDKKNFYSAETILLTNFQNLMAQKQINDF 180
DB 121 HELTQKTQDLKLSIGNTLFIQRLQPKRFLBDKKNFYSAETILLTNFQNLMAQKQINDF 180
QY 181 ISQKTHGKINMLIENIDPGTWMLNANYIFPRARKHGFDPNTYKEDFLEKNSVYKVP 240
DB 181 ISQKTHGKINMLIENIDPGTWMLNANYIFPRARKHGFDPNTYKEDFLEKNSVYKVP 240
QY 241 MERSGIYQGYDQKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
DB 241 MERSGIYQGYDQKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
QY 301 RRVVDVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSKLVGEAVHKAELKM 360
DB 301 RRVVDVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSKLVGEAVHKAELKM 360
QY 361 DERGTGAAGTGAQTLPMTETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPICK 414
DB 361 DERGTGAAGTGAQTLPMTETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPICK 414

RESULT 8
US-10-012-542-134
/ Sequence 134, Application US/10012542
/ Publication No. US20030044851A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 94 Human Secreted Proteins
/ FILE REFERENCE: P2029P1
/ CURRENT APPLICATION NUMBER: US/10/012,542
/ CURRENT FILING DATE: 2001-12-12
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-14
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
/ NUMBER OF SEQ ID NOS: 532
/ SOFTWARE: Patentin Ver. 532
/ SEQ ID NO: 532
/ LENGTH: 532
```

```
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 134
/ LENGTH: 415
/ TYPE: PR
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (415)
/ OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
/ OTHER INFORMATION: acids
US-10-012-542-134

Query Match      100.0%; Score 414; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPFLGLAIFLAVLLTVKGLIKPSFSPRNYKALSEVQGWKORMAAKELARQNMNDLGFKLL 60
DB 1 MNPFLGLAIFLAVLLTVKGLIKPSFSPRNYKALSEVQGWKORMAAKELARQNMNDLGFKLL 60
QY 61 KKLAFNPGNITFLSPLSISTAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHSGFYII 120
DB 61 KKLAFNPGNITFLSPLSISTAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHSGFYII 120
QY 121 HELTQKTQDLKLSIGNTLFIQRLQPKRFLBDKKNFYSAETILLTNFQNLMAQKQINDF 180
DB 121 HELTQKTQDLKLSIGNTLFIQRLQPKRFLBDKKNFYSAETILLTNFQNLMAQKQINDF 180
QY 181 ISQKTHGKINMLIENIDPGTWMLNANYIFPRARKHGFDPNTYKEDFLEKNSVYKVP 240
DB 181 ISQKTHGKINMLIENIDPGTWMLNANYIFPRARKHGFDPNTYKEDFLEKNSVYKVP 240
QY 241 MERSGIYQGYDQKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
DB 241 MERSGIYQGYDQKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
QY 301 RRVVDVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSKLVGEAVHKAELKM 360
DB 301 RRVVDVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSKLVGEAVHKAELKM 360
QY 361 DERGTGAAGTGAQTLPMTETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPICK 414
DB 361 DERGTGAAGTGAQTLPMTETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPICK 414

RESULT 9
US-10-115-123-134
/ Sequence 134, Application US/10115123
/ Publication No. US20030065151A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 94 Human Secreted Proteins
/ FILE REFERENCE: P2029G30AP1D2
/ CURRENT APPLICATION NUMBER: US/10/115,123
/ CURRENT FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: PCT/US99/13418
/ PRIOR FILING DATE: 1999-06-15
/ PRIOR APPLICATION NUMBER: 60/089,507
/ PRIOR FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: 60/089,508
/ PRIOR FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: 60/089,509
/ PRIOR FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: 60/089,510
/ PRIOR FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: 60/090,112
/ PRIOR FILING DATE: 1998-06-22
/ PRIOR APPLICATION NUMBER: 60/090,113
/ PRIOR FILING DATE: 1998-06-22
/ NUMBER OF SEQ ID NOS: 532
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 134
/ LENGTH: 415
```

TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: SITE
LOCATION: (415)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-115-123-134

Query Match 100.0%; Score 414; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVALITVYKGLKPSFSPRNKALSEVQGMKRMAKELARQNMIDGFTLL 60
DB 1 MNPTGLAIFLAVALITVYKGLKPSFSPRNKALSEVQGMKRMAKELARQNMIDGFTLL 60
QY 61 KCLAFYVPGNRIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFFHYI 120
DB 61 KCLAFYVPGNRIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFFHYI 120
QY 121 HELTQKTQDLKLSIGNTLFDQRLQPKRFLDANKFYSAETILTNPONLEMAQKQINDF 180
DB 121 HELTQKTQDLKLSIGNTLFDQRLQPKRFLDANKFYSAETILTNPONLEMAQKQINDF 180
QY 181 ISQKTHGKINNLINIDPGTVMLLANYIFPRARKHEFDPNVTKEBDFLEKNSVYKVP 240
DB 181 ISQKTHGKINNLINIDPGTVMLLANYIFPRARKHEFDPNVTKEBDFLEKNSVYKVP 240
QY 241 MFRSGIYQVGVDDKLSCTIIEIPYQKNITAFILPDEGKLNLEKGLQVDTFSRWKTLIS 300
DB 241 MFRSGIYQVGVDDKLSCTIIEIPYQKNITAFILPDEGKLNLEKGLQVDTFSRWKTLIS 300
QY 301 RRVVDVSVPLHMTGTDLKKTLSYIGVSKIPEEHGDLTKIAPRSILKVGAAVKAELKM 360
DB 301 RRVVDVSVPLHMTGTDLKKTLSYIGVSKIPEEHGDLTKIAPRSILKVGAAVKAELKM 360
QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIGK 414
DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIGK 414

RESULT 10
US-10-800-834-134
Sequence 134, Application US/10800834
Publication No. US20040146930A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029P1D3
CURRENT APPLICATION NUMBER: US/10/800, 834
CURRENT FILING DATE: 2004-03-16
PRIOR APPLICATION NUMBER: 10/115,123
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/461,325
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,508
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,510
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/090,112
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090,113
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 134
LENGTH: 415

TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: SITE
LOCATION: (415)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-800-834-134

Query Match 100.0%; Score 414; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVALITVYKGLKPSFSPRNKALSEVQGMKRMAKELARQNMIDGFTLL 60
DB 1 MNPTGLAIFLAVALITVYKGLKPSFSPRNKALSEVQGMKRMAKELARQNMIDGFTLL 60
QY 61 KCLAFYVPGNRIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFFHYI 120
DB 61 KCLAFYVPGNRIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFFHYI 120
QY 121 HELTQKTQDLKLSIGNTLFDQRLQPKRFLDANKFYSAETILTNPONLEMAQKQINDF 180
DB 121 HELTQKTQDLKLSIGNTLFDQRLQPKRFLDANKFYSAETILTNPONLEMAQKQINDF 180
QY 181 ISQKTHGKINNLINIDPGTVMLLANYIFPRARKHEFDPNVTKEBDFLEKNSVYKVP 240
DB 181 ISQKTHGKINNLINIDPGTVMLLANYIFPRARKHEFDPNVTKEBDFLEKNSVYKVP 240
QY 241 MFRSGIYQVGVDDKLSCTIIEIPYQKNITAFILPDEGKLNLEKGLQVDTFSRWKTLIS 300
DB 241 MFRSGIYQVGVDDKLSCTIIEIPYQKNITAFILPDEGKLNLEKGLQVDTFSRWKTLIS 300
QY 301 RRVVDVSVPLHMTGTDLKKTLSYIGVSKIPEEHGDLTKIAPRSILKVGAAVKAELKM 360
DB 301 RRVVDVSVPLHMTGTDLKKTLSYIGVSKIPEEHGDLTKIAPRSILKVGAAVKAELKM 360
QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIGK 414
DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIGK 414

RESULT 11
US-09-755-665-57
Sequence 57, Application US/09755665
Patent No. US20020107186A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce B.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 361
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: VARIANT
LOCATION: (1) . (361)
OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
US-09-755-665-57

Query Match 74.9%; Score 310; DB 3; Length 361;
Best Local Similarity 100.0%; Pred. No. 4,2e-291;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 DLGFKLLKLAFLNPGNIFLSPISISTAFSMLCLGAODSTLDEIKOGFNFRKPEKDLH 113
DB 1 DLGFKLLKLAFLNPGNIFLSPISISTAFSMLCLGAODSTLDEIKOGFNFRKPEKDLH 60
QY 114 EGFHYIHELTKTODKLSIGNTLFDORLQORKELEDAKNFYSAETILTNFONLEMA 173
DB 61 EGFHYIHELTKTODKLSIGNTLFDORLQORKELEDAKNFYSAETILTNFONLEMA 120
QY 174 QKQINDFISQKTHGKINNLINENIDPGTMLANYIFPRARKHEFDPNVTKEDPFLEKN 233
DB 121 QKQINDFISQKTHGKINNLINENIDPGTMLANYIFPRARKHEFDPNVTKEDPFLEKN 180
QY 234 SSVKVPMMFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLHLEKGLQVDTFS 293
DB 181 SSVKVPMMFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLHLEKGLQVDTFS 240
QY 294 RMTLLSRVVDSVPRLHMTGTFDLKKTLSYIGVSKIFEHGDLTAKAPHSLSKVGAV 353
DB 241 RMTLLSRVVDSVPRLHMTGTFDLKKTLSYIGVSKIFEHGDLTAKAPHSLSKVGAV 300
QY 354 HKAEKMDER 363
DB 301 HKAEKMDER 310

RESULT 12

US-10-629-248-57
Sequence 57, Application US/10629248
Publication No. US20040116671A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhidas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce E.
APPLICANT: Spader, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/10/629,248
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/755,665
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 361
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(361)
OTHER INFORMATION: wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
US-10-629-248-57

Query Match 74.9%; Score 310; DB 4; Length 361;
Best Local Similarity 100.0%; Pred. No. 4,2e-291;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 DLGFKLLKLAFLNPGNIFLSPISISTAFSMLCLGAODSTLDEIKOGFNFRKPEKDLH 113
DB 1 DLGFKLLKLAFLNPGNIFLSPISISTAFSMLCLGAODSTLDEIKOGFNFRKPEKDLH 60
QY 114 EGFHYIHELTKTODKLSIGNTLFDORLQORKELEDAKNFYSAETILTNFONLEMA 173
DB 61 EGFHYIHELTKTODKLSIGNTLFDORLQORKELEDAKNFYSAETILTNFONLEMA 120
QY 174 QKQINDFISQKTHGKINNLINENIDPGTMLANYIFPRARKHEFDPNVTKEDPFLEKN 233
DB 121 QKQINDFISQKTHGKINNLINENIDPGTMLANYIFPRARKHEFDPNVTKEDPFLEKN 180

DB 121 QKQINDFISQKTHGKINNLINENIDPGTMLANYIFPRARKHEFDPNVTKEDPFLEKN 180
QY 234 SSVKVPMMFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLHLEKGLQVDTFS 293
DB 181 SSVKVPMMFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLHLEKGLQVDTFS 240
QY 294 RMTLLSRVVDSVPRLHMTGTFDLKKTLSYIGVSKIFEHGDLTAKAPHSLSKVGAV 353
DB 241 RMTLLSRVVDSVPRLHMTGTFDLKKTLSYIGVSKIFEHGDLTAKAPHSLSKVGAV 300
QY 354 HKAEKMDER 363
DB 301 HKAEKMDER 310

RESULT 13

US-10-276-774-2202
Sequence 2202, Application US/10276774
Publication No. US20040053245A1
GENERAL INFORMATION:
APPLICANT: Hybreg, Inc.
APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 2202
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
US-10-276-774-2202

Query Match 43.7%; Score 181; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 3,8e-166;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLTVKGLKPSFPNNYKALSEVQGNKQMAKELARQNNDLGFKLL 60
DB 18 MNPTGLAIFLAVLTVKGLKPSFPNNYKALSEVQGNKQMAKELARQNNDLGFKLL 77
QY 61 KCLAFNPGNIFLSPISISTAFSMLCLGAODSTLDEIKOGFNFRKPEKDLHEGFHYII 120
DB 78 KCLAFNPGNIFLSPISISTAFSMLCLGAODSTLDEIKOGFNFRKPEKDLHEGFHYII 137
QY 121 HELTKTODKLSIGNTLFDORLQORKELEDAKNFYSAETILTNFONLEMAQKQINDF 180
DB 138 HELTKTODKLSIGNTLFDORLQORKELEDAKNFYSAETILTNFONLEMAQKQINDF 197
QY 181 I 181
DB 198 I 198

RESULT 14

US-09-864-761-48438
Sequence 48438, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23

```

; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48438
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL132708.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: P50447, EVALU8 8.00e-28
; OTHER INFORMATION: EST_HUMAN HIT: AV649144.1, EVALU8 3.00e-27
; US-09-864-761-48438

```

```

Query Match 31.2%; Score 129; DB 3; Length 140;
Best Local Similarity 100.0%; Pred. No. 3e-116;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 FSWLCLGADSTLDEIKGQNFPRKMPKDIHSGFYIHELTKOTDCLKISGNTLFTDQ 142
DB 1 FSWLCLGADSTLDEIKGQNFPRKMPKDIHSGFYIHELTKOTDCLKISGNTLFTDQ 60

QY 143 RLDPORRFLDANFYSAETILTNFONLEMAKQINDPISQKTHGKINNLINENIDPQW 202
DB 61 RLDPORRFLDANFYSAETILTNFONLEMAKQINDPISQKTHGKINNLINENIDPQW 120

QY 203 LLANYIFPR 211
DB 121 LLANYIFPR 129

```

Search completed: March 31, 2006, 10:13:53
Job time : 121.26 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 10:10:05 ; Search time 16.8875 Seconds
(without alignments)
746.288 Million cell updates/sec

Title: US-10-664-356-1562

Perfect score: 414

Sequence: 1 MNPTLGIATFIATVLTAKL.....YSEKIPSVLFIKIVNPIGK 414

Scoring matrix: BLO62

Gapop 60.0 , Gapext 60.0

Searched: 180808 seqs, 30441898 residues

Word size: 35

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Published Applications_AA_New:*

- 1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 5: /SIDS5/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
- 6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	ID	Description

No matches found

Search completed: March 31, 2006, 10:14:30
Job time : 16.8875 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:54:55 ; Search time 210.927 Seconds
(without alignments)
822.818 Million cell updates/sec

Title: US-10-664-356-1562_COPY_20_414
Perfect score: 395
Sequence: 1 LTKPSFSPRYKALSEVQGW.....YSEKIPSVLFLGKIVNPIGK 395

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 15

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	395	100.0	414	4 AAU05754	AAU05754 Human NOV
2	395	100.0	414	4 AAE04885	AAE04885 Human pro
3	395	100.0	414	6 ADA57300	ADA57300 Human sec
4	395	100.0	414	6 ADA41179	ADA41179 Human sec
5	395	100.0	414	8 ADN05952	ADN05952 Antipsoi
6	395	100.0	415	3 AAY86217	AAY86217 Human sec
7	395	100.0	415	6 ABO53360	ABO53360 Novel hum
8	334	84.6	414	4 AAM78898	AAM78898 Human pro
9	310	78.5	358	4 AAU05759	AAU05759 Human NOV
10	170	43.0	431	4 ABB11832	ABB11832 Human sec
11	170	43.0	431	4 AAM79882	AAM79882 Human pro
12	129	32.7	140	4 AAM70426	AAM70426 Human bon

ALIGNMENTS

RESULT 1
AAU05754
ID AAU05754 standard; protein; 414 AA.
XX AAU05754;
XX
XX 24-OCT-2001 (first entry)

XX	Human NOV polypeptide.
DE	
XX	Human, NOV7; AL132990 B; fertility disorder; spermatogenesis; cardiac;
XX	cytostatic; immunomodulatory; antiproliferative; antidiabetic;
KW	cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
KW	pulmonary disorder; haematopoietic disorder; immunological disorder;
KW	inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
KW	wound healing; gene therapy.
OS	Homo sapiens.
XX	
XX	MO200149729-A2.
XX	
PD	12-JUL-2001.
XX	
XX	05-JAN-2001; 2001WO-US000299.
PF	
XX	06-JAN-2000; 2000US-0174724P.
PR	11-JAN-2000; 2000US-0175434P.
PR	11-JAN-2000; 2000US-0175488P.
PR	12-JAN-2000; 2000US-0175696P.
PR	12-JAN-2000; 2000US-0175743P.
PR	13-JAN-2000; 2000US-0175819P.
PR	07-AUG-2000; 2000US-0223524P.
PR	04-JAN-2001; 2001US-0075565S.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Prayaga SK, Majumder K, Taillon BE, Spaderna SK, Spytek KA;
PI	MacDougall J;
XX	
DR	WPI, 2001-418356/44.
DR	N-PSDB; AAS10874.
XX	
PT	Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
PT	for treating a syndrome associated with a NOVX-associated disorder, e.g.
PT	cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
PT	pulmonary disorder.
XX	
PS	Claim 1; Page 32; 14pp; English.
XX	
CC	The invention relates to nucleic acids encoding NOVX (X being an integer
CC	from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
CC	useful in diagnosing, treating or manufacturing a medicament for a
CC	disease or disorder associated with NOVX e.g. cell proliferation (cancer
CC	and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
CC	disorders (e.g. of spermatogenesis), haematopoietic, immunological,
CC	inflammatory and tumour related disorders, emphysema, cirrhosis, wound
CC	healing. NOVX nucleic acids are also useful in gene therapy. They are
CC	also used for screening for a modulator of activity or of latency or
CC	predisposition to a NOVX-associated disorder. They are also useful for
CC	determining the presence of or predisposition to a NOVX-associated
CC	disorder. The present sequence represents NOV7 (AL132990 B), which has
CC	sequence homology to an unidentified human secreted protein (HMHGUS54)
CC	and to alpha anti-trypsin
XX	
SQ	Sequence 414 AA;
XX	
Query Match	100.0%; Score 395; DB 4; Length 414;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 395; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 LTKPSFSPRYKALSEVQGWKQMAKELARQNDLGFKLKKLAAPNPNRNIFLSPLSI 60
DB	20 LTKPSFSPRYKALSEVQGWKQMAKELARQNDLGFKLKKLAAPNPNRNIFLSPLSI 79
QY	61 STAFSMLCAGADSTIDEIKQGNFPRKMPKDLHSGFTYIHLELTQTDKLSIGNTLF 120
DB	80 STAFSMLCAGADSTIDEIKQGNFPRKMPKDLHSGFTYIHLELTQTDKLSIGNTLF 139
QY	121 IDQRLQRFLEDAKNFYSAETITLTFNFOLEMAQKQINDFISQKHGKNNLEINIDPG 180

XX MO2002102994-A2.
 XX 27-DEC-2002.
 XX 19-MAR-2002; 2002MO-US008278.
 XX 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 XX WPI: 2003-167512/16.
 DR N-PSDB; ADA56404.
 XX
 PT New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.
 PS
 PS Claim 13; SEQ ID NO 1490; 1754pp; English.
 XX
 CC The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid
 CC sequence at least 95% identical to the new sequences. The polypeptides,
 CC antibodies or antibody fragments that bind to the polypeptides, nucleic
 CC acids encoding the polypeptides, agonists or antagonists that binds to
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
 CC compositions for diagnosing, treating or preventing an e.g. immune
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 CC hepatitis or Crohn's disease), respiratory disorders (e.g. asthma and
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
 CC polynucleotides are useful for chromosome identification, chromosome
 CC mapping, for controlling gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals
 CC from minute biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful for as molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for
 CC treating or preventing neural disorders, immune system disorders,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds
 CC to one of the polypeptide of the invention. Note: This sequence corresponds
 CC to this patent did form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 414 AA:
 Query Match 100.0%; Score 395; DB 6; Length 414;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNKSPSPRYKXKLSVQGMKORMAKELARONMDLGFKLLKQLAFNPGRNIFLPLSLI 60
 DB 20 LNKSPSPRYKXKLSVQGMKORMAKELARONMDLGFKLLKQLAFNPGRNIFLPLSLI 79
 QY 61 STAFSMCLGADSTLDEIKGFNFRMPKDLHGFHYIHLVYQTKODLKLSIGNTLP 120
 DB 80 STAFSMCLGADSTLDEIKGFNFRMPKDLHGFHYIHLVYQTKODLKLSIGNTLP 139
 QY 121 IDRLQPKRFLBDANKFYSAETILTNFQULEMAOKINDPISGKTHGKINNTLENTDPG 180
 DB 140 IDRLQPKRFLBDANKFYSAETILTNFQULEMAOKINDPISGKTHGKINNTLENTDPG 199

QY 181 TWMLANYIFRRARMKHEPDNPVTKEDPFLERKNSVYKVMRSGIYQGYDJKLSTCI 240
 DB 200 TWMLANYIFRRARMKHEPDNPVTKEDPFLERKNSVYKVMRSGIYQGYDJKLSTCI 259
 QY 241 LEIPYQKNITATITLPDEGKLKHEKGLQYDTSRMKTLLSRVVDVSVPLMHTGTFDL 300
 DB 260 LEIPYQKNITATITLPDEGKLKHEKGLQYDTSRMKTLLSRVVDVSVPLMHTGTFDL 319
 QY 301 KKTLSYIGVSKIFEEHGDLTAKIAPHSLKYGEAVHKAELQMDRSGTEGAAGTQTPME 360
 DB 320 KKTLSYIGVSKIFEEHGDLTAKIAPHSLKYGEAVHKAELQMDRSGTEGAAGTQTPME 379
 QY 361 TPLVVKIDKPEYLLIYSEKIPSVLFLGKIYVPIGK 395
 DB 380 TPLVVKIDKPEYLLIYSEKIPSVLFLGKIYVPIGK 414
 RESULT 4
 ADA41179
 ID ADA41179 standard; protein; 414 AA.
 XX
 AC ADA41179;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted protein.
 XX
 KW Human; secreted protein; cancer; hyperproliferative disorder;
 KW rheumatoid arthritis; autoimmune disorder; hematopoietic disorder;
 KW anaemia; allergic reaction; asthma; cardiovascular disorder;
 KW wound healing; cystostatic; immunosuppressive; nocotropic; neuroprotective;
 KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
 KW vulnereary; cardiant; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN MO2002102993-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002MO-US008123.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 XX
 XX WPI: 2003-175238/17.
 DR
 XX
 PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.
 XX
 PS Claim 1; SEQ ID NO 1561; 3205pp; English.
 XX
 CC The invention relates to novel genes ADA39629-ADA40565 and proteins
 CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting,
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 CC anaemia), hematopoietic or hematological disorders (e.g. anaemia,
 CC thrombocytopenia), allergic reactions including asthma or eczema,

CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences.

SQ Sequence 414 AA;

Query Match 100.0%; Score 395; DB 6; Length 414;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKSPSPRYKALSEVQGMKQMAKELARQNMDFGLKKLAFYNGRNIPLSPST 60
DB LKSPSPRYKALSEVQGMKQMAKELARQNMDFGLKKLAFYNGRNIPLSPST 79
QY 61 STAFSMLCIGAODSTLDEIKQGFNFRKMPKDLHEGFHYIHELTKTODLKLSIGNTLF 120
DB STAFSMLCIGAODSTLDEIKQGFNFRKMPKDLHEGFHYIHELTKTODLKLSIGNTLF 139
QY 121 IDORLOPQKFLDANKFYSAETITLNFQNLMAQKQINDFISQTHGKINNLINIDPG 180
DB IDORLOPQKFLDANKFYSAETITLNFQNLMAQKQINDFISQTHGKINNLINIDPG 199
QY 181 TWMLANTYFFPRARWHEPDNVTKEEDFLEKNSVKKVPMFRSGIYGVYDDKLSCTI 240
DB TWMLANTYFFPRARWHEPDNVTKEEDFLEKNSVKKVPMFRSGIYGVYDDKLSCTI 259
QY 241 LEIPYQKNTAIFILPDEGKLKHEKGLQVDFSRWKTLLSRVVDVSVRLHMTGTFDL 300
DB LEIPYQKNTAIFILPDEGKLKHEKGLQVDFSRWKTLLSRVVDVSVRLHMTGTFDL 319
QY 301 KKTLSYIGVSKIFEEHGDLTAKAPHRSLKVGSAVHKAELKMDERGTEGAAGTGLPME 360
DB KKTLSYIGVSKIFEEHGDLTAKAPHRSLKVGSAVHKAELKMDERGTEGAAGTGLPME 379
QY 361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 395
DB TPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 414

RESULT 5
ADN05952
ID ADN05952 standard; protein; 414 AA.

AC ADN05952;

DT 01-JUL-2004 (first entry)

DE Antipsoriatic protein sequence #1136.

KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX Homo sapiens.

XX MO2004028479-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030907.

XX 25-SEP-2002; 2002US-0414006P.

XX (GETH) GENENTECH INC.

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WR;
PI Wu TD;
XX
XX WPI; 2004-305105/28.
DR N-PDB; ADN05951.

PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.

PS Claim 9; SEQ ID NO 2347; 3069pp; English.

CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.

SQ Sequence 414 AA;

Query Match 100.0%; Score 395; DB 8; Length 414;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKSPSPRYKALSEVQGMKQMAKELARQNMDFGLKKLAFYNGRNIPLSPST 60
DB LKSPSPRYKALSEVQGMKQMAKELARQNMDFGLKKLAFYNGRNIPLSPST 79
QY 61 STAFSMLCIGAODSTLDEIKQGFNFRKMPKDLHEGFHYIHELTKTODLKLSIGNTLF 120
DB STAFSMLCIGAODSTLDEIKQGFNFRKMPKDLHEGFHYIHELTKTODLKLSIGNTLF 139
QY 121 IDORLOPQKFLDANKFYSAETITLNFQNLMAQKQINDFISQTHGKINNLINIDPG 180
DB IDORLOPQKFLDANKFYSAETITLNFQNLMAQKQINDFISQTHGKINNLINIDPG 199
QY 181 TWMLANTYFFPRARWHEPDNVTKEEDFLEKNSVKKVPMFRSGIYGVYDDKLSCTI 240
DB TWMLANTYFFPRARWHEPDNVTKEEDFLEKNSVKKVPMFRSGIYGVYDDKLSCTI 259
QY 241 LEIPYQKNTAIFILPDEGKLKHEKGLQVDFSRWKTLLSRVVDVSVRLHMTGTFDL 300
DB LEIPYQKNTAIFILPDEGKLKHEKGLQVDFSRWKTLLSRVVDVSVRLHMTGTFDL 319
QY 301 KKTLSYIGVSKIFEEHGDLTAKAPHRSLKVGSAVHKAELKMDERGTEGAAGTGLPME 360
DB KKTLSYIGVSKIFEEHGDLTAKAPHRSLKVGSAVHKAELKMDERGTEGAAGTGLPME 379
QY 361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 395
DB TPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 414

RESULT 6
AAH6217
ID AAH6217 standard; protein; 415 AA.

AC AAH6217;

DT 19-APR-2000 (first entry)

DE Human secreted protein HMHG54, SEQ ID NO:132.

KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy.

XX Homo sapiens.

XX MO9966041-A1.
 XX 23-DEC-1999.
 XX
 XX 15-JUN-1999; 99MO-US013418.
 XX 16-JUN-1998; 98US-0089507P.
 XX 16-JUN-1998; 98US-0089508P.
 XX 16-JUN-1998; 98US-0089509P.
 XX 16-JUN-1998; 98US-0089510P.
 XX 22-JUN-1998; 98US-0090112P.
 XX 22-JUN-1998; 98US-0090113P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA,
 PI Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R,
 PI Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsoulis G;
 XX MPI; 2000-106100/09.
 XX N-PSDB; AA297021.
 XX
 XX New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 XX
 XX Claim 1; Page 389-390; 586pp; English.
 XX
 XX AA297019 to AA297137 represent 94 isolated human secreted protein genes.
 CC AA297019 to AA297137 are the secreted proteins encoded by the 94 human
 CC genes. This sequence represents a fragment of one of the human secreted
 CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions, e.g.,
 CC by protein or gene therapy. Also pathological conditions can be diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new genes. Specific uses are
 CC described for each of the 94 genes, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, tumours, developmental abnormalities and foetal
 CC deficiencies, blood disorders, diseases of the immune system, autoimmune
 CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
 CC schistosomiasis, arthritis, asthma, psoriasis, sepsis, skin disorders,
 CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
 CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
 CC also useful for identifying their binding partners. The sequences shown
 CC in AA297019 to AA297137 represent fragments of the secreted proteins
 CC
 XX
 XX Sequence 415 AA:
 SQ
 Query Match 100.0%; Score 395; DB 3; Length 415;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 KTLSTYIGVSKIPFEHNDLTKIAPHRSKLVGEAVHKAELKMDERGTGAAGTQTPME 360
 DB 320 KTLSTYIGVSKIPFEHNDLTKIAPHRSKLVGEAVHKAELKMDERGTGAAGTQTPME 379
 QY 361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIVNPICK 395
 DB 380 TPLVVKIDKPYLLIYSEKIPSVLFLGKIVNPICK 414
 RESULT 7
 ID ABO53360 standard; protein; 415 AA.
 XX ABO53360;
 AC
 XX ABO53360;
 DT 06-NOV-2003 (first entry)
 XX
 XX Novel human secreted protein #3.
 XX
 XX Human; vaccine; immune system disorder; haematopoietic cell disorder;
 KW cancer; autoimmune disorder; rheumatoid arthritis; glomerulonephritis;
 KW HIV infection; anaemia; thrombocytopenia blood coagulation disorder;
 KW blood platelet disorder; wound; heart attack; myocardial infarction;
 KW stroke; scarring; asthma; graft-versus host rejection; inflammation;
 KW hyperproliferative disorder; lymphoproliferative disorder; arrhythmia;
 KW aberrant cellular division; cell proliferative disorder; angiogenesis;
 KW cardiovascular disorder; pulmonary heart disease; neovascularisation;
 KW hypertrophic scar; keloid; ocular disorder; diabetic retinopathy;
 KW uveitis; epithelial cell proliferation; neurological disease; apoptosis;
 KW Parkinson's disease; Alzheimer's disease; Huntington's chorea; AIDS; AIDS;
 KW amyotrophic lateral sclerosis; toxin induced liver disease; septic shock;
 KW cachexia; anorexia; lung damage; infection.
 XX
 OS Homo sapiens.
 XX
 XX US2003065151-A1.
 XX
 XX 03-APR-2003.
 XX
 XX 04-APR-2002; 2002US-00115123.
 XX
 XX 16-JUN-1998; 98US-0089507P.
 XX 16-JUN-1998; 98US-0089508P.
 XX 16-JUN-1998; 98US-0089509P.
 XX 16-JUN-1998; 98US-0089510P.
 XX 22-JUN-1998; 98US-0090112P.
 XX 22-JUN-1998; 98US-0090113P.
 XX 15-JUN-1999; 99MO-US013418.
 XX 14-DEC-1999; 99US-00461325.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Ni J, Rosen CA, Wei Y, Young P, Florence K, Soppet DR,
 PI Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R, Lafleur DW,
 PI Olsen H, Shi Y, Moore PA, Komatsoulis G;
 XX MPI; 2003-531736/50.
 XX N-PSDB; ACH66650.
 XX
 XX Novel antibody that binds specifically to a HCE3069 protein, useful for
 PT detecting the presence of a protein in a biological sample, and for
 PT treating cancers, autoimmune disorders and HIV infection.
 XX
 XX Disclosure; SEQ ID NO 134; 176pp; English.
 XX
 XX The invention relates to an isolated antibody or its fragment that
 CC specifically binds to a protein. The antibody is useful for detecting a
 CC protein in a biological sample, by contacting the biological sample with
 CC the antibody or its fragment and detecting the protein in the biological
 CC sample. The antibody is useful for purifying, detecting and targeting the
 CC human secreted proteins, including both in vitro and in vivo diagnostic
 CC and therapeutic methods. The antibody is useful for immunophenotyping of

cell lines in biological samples and in antibody-based therapies for treating, inhibiting and preventing diseases, disorders or conditions associated with aberrant expression and/or activity of the above proteins. The antibody is useful for treating deficiencies or disorders of immune system and haematopoietic cells, for increasing differentiation and proliferation of haematopoietic cells, for treating immune deficiencies or disorders e.g. cancers, autoimmune disorders (such as rheumatoid arthritis and glomerulonephritis), HIV infection, anaemia and thrombocytopenia and as a marker for a particular immune system disease or disorder. The antibody is also useful for treating blood coagulation disorders, blood platelet disorders, wounds, heart attacks (infarction), strokes, scarring and asthma. The antibody is also useful for treating or preventing graft-versus host rejection, for modulating inflammation, for treating hyperproliferative disorders e.g. lymphoproliferative disorders and cancers, for inhibiting aberrant cellular division and for treating cell proliferative disorders. The antibody is also useful for treating cardiovascular disorders e.g. pulmonary heart disease and arrhythmia, disorders associated with neovascularization and angiogenesis, for treating hypertrophic scars and keloids, ocular disorders e.g. diabetic retinopathy and uveitis, for wound healing and disorders of epithelial cell proliferation. The antibody is also useful for treating neurological diseases e.g. Parkinson's disease, Alzheimer's disease, Huntington's chorea and amyotrophic lateral sclerosis (ALS), diseases associated with increased apoptosis e.g. AIDS, toxin induced liver disease, septic shock, cachexia and anorexia, for preventing and healing damage to lungs and for treating infectious diseases. The present sequence represents the amino acid sequence of a novel human secreted protein. Note: the sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docId=2003065151

XX Sequence 415 AA;

Query Match 100.0%; Score 395; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPSFSPNNRYALSEVOGKQMAKELARQNDLGFLLKCLAFYNGRNIFLSPLSI 60
DB 20 LKPSFSPNNRYALSEVOGKQMAKELARQNDLGFLLKCLAFYNGRNIFLSPLSI 79
QY 61 STRFSLCIGADSTLDEIKQGFNRKMPKOLHGFHYIHELTKQTDKLSIGNTLF 120
DB 80 STRFSLCIGADSTLDEIKQGFNRKMPKOLHGFHYIHELTKQTDKLSIGNTLF 139
QY 121 IDORLOPQRKFLBDANKFYSAETILTNFONLEMAQKQINDFISQKTHGINNLIENIDG 180
DB 140 IDORLOPQRKFLBDANKFYSAETILTNFONLEMAQKQINDFISQKTHGINNLIENIDG 199
QY 181 TWMLANTYIFPRARWGHEDPNVTKEEDFLEKNSSVQVPMFRSGIYQGYDDKLSCTI 240
DB 200 TWMLANTYIFPRARWGHEDPNVTKEEDFLEKNSSVQVPMFRSGIYQGYDDKLSCTI 259
QY 241 LBIPLYOKNTTAIFILPDEGKLKLEKGLQVDTFSRKTTLSRRVVDVSPRLMTGTFFDL 300
DB 260 LBIPLYOKNTTAIFILPDEGKLKLEKGLQVDTFSRKTTLSRRVVDVSPRLMTGTFFDL 319
QY 301 KKTLSYIGVSKTPEBHGDLTKIAPHRSLLKVGSAVHAAELKMBDRGEGAAGTLPME 360
DB 320 KKTLSYIGVSKTPEBHGDLTKIAPHRSLLKVGSAVHAAELKMBDRGEGAAGTLPME 379
QY 361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
DB 380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414

RESULT 8

AAM78898

XX AAM78898 standard; protein; 414 AA.

AC AAM78898;

XX 06-NOV-2001 (first entry)

XX Human protein SEQ ID NO 1560.
DE
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
PN MO200157190-A2.
XX

PD 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US004098.

XX 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

XX (HYSB-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
DR N-PSDB; AAK52031.XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
XX Claim 20; Page 3878-3879; 6221pp; English.

PS The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoietic regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX

XX Sequence 414 AA;

Query Match 84.6%; Score 334; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPSFSPNNRYALSEVOGKQMAKELARQNDLGFLLKCLAFYNGRNIFLSPLSI 60
DB 20 LKPSFSPNNRYALSEVOGKQMAKELARQNDLGFLLKCLAFYNGRNIFLSPLSI 79
QY 61 STRFSLCIGADSTLDEIKQGFNRKMPKOLHGFHYIHELTKQTDKLSIGNTLF 120
DB 80 STRFSLCIGADSTLDEIKQGFNRKMPKOLHGFHYIHELTKQTDKLSIGNTLF 139
QY 121 IDORLOPQRKFLBDANKFYSAETILTNFONLEMAQKQINDFISQKTHGINNLIENIDG 180
DB 140 IDORLOPQRKFLBDANKFYSAETILTNFONLEMAQKQINDFISQKTHGINNLIENIDG 199
QY 181 TWMLANTYIFPRARWGHEDPNVTKEEDFLEKNSSVQVPMFRSGIYQGYDDKLSCTI 240
DB 200 TWMLANTYIFPRARWGHEDPNVTKEEDFLEKNSSVQVPMFRSGIYQGYDDKLSCTI 259

DB 200 TVALNANYIFFRARWKHEFPDNTKEDPFLERKNSVYKVPMMFRSGIYQVYDCKLSCTI 259
 QY 241 LEIPYQKNITAIPIPLPEEGKLKHLKEGLQVDTSSRMKTLISRRVVDVSVPLHMTGFDL 300
 DB 260 LEIPYQKNITAIPIPLPEEGKLKHLKEGLQVDTSSRMKTLISRRVVDVSVPLHMTGFDL 319
 QY 301 KKTLSYIGVSKIFEBHGDLTFKIAPHRSKLVGEAV 334
 DB 320 KKTLSYIGVSKIFEBHGDLTFKIAPHRSKLVGEAV 353

RESULT 9
 AAU05759
 ID AAU05759 standard; protein; 358 AA.
 XX
 AC AAU05759;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human NOV7 polypeptide #2.
 XX
 KM Human: NOV7; A1132990 B; fertility disorder; spermatogenesis; cardiant;
 KM cyrostatic; immunomodulatory; antiproliferative; antidiabetic;
 KM cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
 KM pulmonary disorder; haematopoietic disorder; immunological disorder;
 KM inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
 KM wound healing; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 311..322
 FT /label= OTHER
 FT /note= "Other= Unknown"
 XX
 PN W0200149729-A2.
 XX
 PD 12-JUL-2001.
 XX
 PP 05-JAN-2001; 2001MO-US000299.
 XX
 PR 06-JAN-2000; 2000US-0174724P.
 PR 11-JAN-2000; 2000US-0175434P.
 PR 11-JAN-2000; 2000US-0175488P.
 PR 12-JAN-2000; 2000US-0175696P.
 PR 12-JAN-2000; 2000US-0175743P.
 PR 13-JAN-2000; 2000US-0175819P.
 PR 07-AUG-2000; 2000US-0223524P.
 PR 04-JAN-2001; 2001US-00755665.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Prayaga SK, Majumder K, Tallon BE, Spaderna SK, Spytek KA;
 PI Macdougall J;
 XX
 DR WPI; 2001-418356/44.
 XX
 PT Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
 PT for treating a syndrome associated with a NOVX-associated disorder, e.g.
 PT cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
 PT pulmonary disorder.
 XX
 PS Disclosure; Page 33; 14pp; English.
 XX
 CC The invention relates to nucleic acids encoding NOVX (X being an integer
 CC from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
 CC useful in diagnosing, treating or manufacturing a medicament for a
 CC disease or disorder associated with NOVX e.g. cell proliferation (cancer
 CC and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
 CC disorders (e.g. of spermatogenesis), haematopoietic, immunological,
 CC inflammatory and tumour related disorders, emphysema, cirrhosis, wound
 CC healing. NOVX nucleic acids are also useful in gene therapy. They are
 CC also used for screening for a modulator of activity or of latency or

CC predisposition to a NOVX-associated disorder. They are also useful for
 CC determining the presence of or predisposition to a NOVX-associated
 CC disorder. The present sequence represents a version of NOV7 (A1132990 B)
 CC appearing in table 25 of the specification, which has sequence homology
 CC to an unidentified human secreted protein (HMGUS54) and to alpha anti-
 CC trypsin
 XX
 SQ Sequence 358 AA;
 XX
 Query Match 78.5%; Score 310; DB 4; Length 358;
 Best Local Similarity 100.0%; Pred. No. 1.4e-299;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 DLGFKLLKTLAIPNPNRIPLSPSTASTAPSMCLGADOSTLDEIRQGFNFRMPKEDLH 94
 DB 1 DLGFKLLKTLAIPNPNRIPLSPSTASTAPSMCLGADOSTLDEIRQGFNFRMPKEDLH 60
 QY 95 EGFHYIHLTQKTDKLSIGNTLFDQRLQPKRFLBDKKNFYSAFTILTNFQULEMA 154
 DB 61 EGFHYIHLTQKTDKLSIGNTLFDQRLQPKRFLBDKKNFYSAFTILTNFQULEMA 120
 QY 155 OKQINDPISQKTHGKINNTLIENTDPTWMLANYIFFRARKHEFPDNTKEDPFLERKN 214
 DB 121 OKQINDPISQKTHGKINNTLIENTDPTWMLANYIFFRARKHEFPDNTKEDPFLERKN 180
 QY 215 SSVKVPMMFRSGIYQVYDCKLSCTILEIPIYQKNITAIPIPLPEEGKLKHLKEGLQVDTFS 274
 DB 181 SSVKVPMMFRSGIYQVYDCKLSCTILEIPIYQKNITAIPIPLPEEGKLKHLKEGLQVDTFS 240
 QY 275 RKMTLSRRVVDVSVPLHMTGFDLTKTLYIGVSKIFEBHGDLTFKIAPHRSKLVGEAV 334
 DB 241 RKMTLSRRVVDVSVPLHMTGFDLTKTLYIGVSKIFEBHGDLTFKIAPHRSKLVGEAV 300
 QY 335 HKAEKLMRDER 344
 DB 301 HKAEKLMRDER 310

RESULT 10
 ABB11832
 ID ABB11832 standard; peptide; 431 AA.
 XX
 AC ABB11832;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human secreted protein homologue, SEQ ID NO:2202.
 XX
 DE Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KM haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KM inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
 KM proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KM chronic inflammatory condition; proliferative retinopathy;
 KM atherosclerosis; coronary heart disease; arterial ischaemia;
 KM bone disorder; osteoporosis; vascular growth disorder;
 KM tissue regeneration; wound healing; infection; immune disorder;
 KM cell culture; drug screening; gene therapy; antiinflammatory;
 KM antisthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KM cyrostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KM antifungal; vulnery; antilulcer.
 XX
 OS Homo sapiens.
 XX
 PN W0200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PP 05-FEB-2001; 2001MO-US003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX

Db 321 VDVSVPRLLMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRS LKVGAV 370

RESULT 12

ID	AA	standard; protein; 140 AA.
xx		

AC AAM70426;

DT 06-NOV-2001 (first entry)

Human bone marrow expressed probe encoded protein SEQ ID NO: 30732.

KM Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.

388

Homo sapiens.

PN W0200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.
VY

PB 04-FEB-2000; 2000US-0180312P.
PB 36-MAY-2000; 2000TC 020745C.

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-0063375C
PR 03-AUG-2000; 2000US-0063375C

PR 21-SBP-2000; 2000US-0234687P.
 DP 27-SBP-2000; 2000US-0234350P

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS IN
XX

Penn SG, Hanzel DK, Chen W, et al.

DR WPI; 2001-488900/53.
XX

PT human genome-derived single exon gene expression in human bone

XX
PS
Example 4: SEO ID NO 30733. 666

The present invention provides

probes which are derived from bone marrow. They can be used

samples, which may enable the identification of such asymbiotic populations.

protein encoded by one of the p

SQ Sequence 140 AA;

Query Match	32.7%; SC
Best Local Similarity	100.0%; F

Matches 129; Conservative 0;

64 RSMCLGAQDSTLDBIKOGFNE

DB 1 KSMLECGAQDSTLDEIKQGFNE

124 RLQPORPLEDAKNFYSAETIL

DB 61 RLQPQRKFLBDKCNFYSAETIL

184 LEANYL PER 192

121 LEANIER 129

Search completed: March 31, 2006. 10

RC28 / 24.717 : 2017 000

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 10:02:58 ; Search time 24.9011 Seconds
(without alignments)
1526.262 Million cell updates/sec

Title: US-10-664-356-1562_COPY_20_414
Perfect score: 395
Sequence: 1 LTKPSFSPRYKALSRVQW.....YSEKIPSVLFGKIVNPIGK 395

Scoring table: ORIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 15

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : PIR_80: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: March 31, 2006, 10:08:39
Job time : 24.9011 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: March 31, 2006, 09:55:21 ; Search time 149.895 Seconds
(without alignments)
1859.193 Million cell updates/sec

Title: US-10-664-356-1562_COPY_20_414
Perfect score: 395
Sequence: 1 LKPSFSPRYKALSEVQW.....YSEKIPSVLFLGIKIVNPIGK 395

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 15

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database :

UniProt_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	395	100.0	414	Q81W75_HUMAN	Q81W75 homo sapien
2	19	4.8	413	Q7TWF5_MOUSE	Q7TWF5 mus musculu
3	19	4.8	413	Q9CGJ2_MOUSE	Q9CGJ2 m mus muscu
4	19	4.8	413	Q6P6M3_MOUSE	Q6P6M3 mus musculu
5	16	4.1	411	Q8R4Z1_RAT	Q8R4Z1 ratu

ALIGNMENTS

RESULT 1
Q81W75_HUMAN
ID Q81W75_HUMAN PRELIMINARY; PRT; 414 AA.
AC Q81W75;
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 13-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1
DE antiprotease, antitrypsin), member 12 (Ol-64) (Visceral adipose-
DE specific SERPIN12).
GN Name=SERPIN12;
OS Homo sapiens (human).
OC Bkaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinetti P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Foley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young J.W., Green B.D., Shvachenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.S., Jones S.U.M., Maira M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences".
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Skin;
RC NIH WGC Project;
RG Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RL [3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Heart;
RC Chen S., Guo J.H., Yu L.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RA NUCLEOTIDE SEQUENCE.
RP Hida K., Wada J., Zhang H.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: Belongs to the serpin family.
DR EMBL: BC040857; AA040857.1; -; mRNA.
DR EMBL: AY177692; AA018649.1; -; mRNA.
DR HSSP: P01009; IOMB.
DR Ensembl: ENSG00000165953; Homo sapiens.
DR HGNC: HGNC:18359; SERPIN12.
DR GO: GO:0004867; F: serine-type endopeptidase inhibitor activity, ISA.
DR InterPro: IPR000215; Prot_inh_serpin.
DR Pfam: PF00079; Serpin_1.
DR SMART: SM00093; SERPIN_1.
KM Serpin.
SQ SEQUENCE 414 AA; 47175 MW; 5C70FLAB5935661C CRC64;
Query Match 100.0%; Score 395; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKPSFSPRYKALSEVQWKQMAAKELARQNDLGFKLKKLAFFNPGNIFLSPLSI 60
DB 20 LKPSFSPRYKALSEVQWKQMAAKELARQNDLGFKLKKLAFFNPGNIFLSPLSI 79
QY 61 STAFSMICGAOSTLDEIKQGFNFRMPKDLHGGHYIHLTQTDLSIGNTLF 120
DB 80 STAFSMICGAOSTLDEIKQGFNFRMPKDLHGGHYIHLTQTDLSIGNTLF 139
QY 121 IDPRLPQRFKLELDANKFYSAETILTNFQNLMAQKQINDFSQKTHGKNNLIENTDPG 180
DB 140 IDPRLPQRFKLELDANKFYSAETILTNFQNLMAQKQINDFSQKTHGKNNLIENTDPG 199
QY 181 TWMLLANYFFRRARWGHEDPNTYKEDDFLEKSSVVKPMFRSGIYQGYDCLKSCTI 240
DB 200 TWMLLANYFFRRARWGHEDPNTYKEDDFLEKSSVVKPMFRSGIYQGYDCLKSCTI 259
QY 241 LRIPIQKNTATIFILDEGLKLEKGLQVDTSSRKTTLSRPVNVSVRLMTGFDL 300
DB 260 LRIPIQKNTATIFILDEGLKLEKGLQVDTSSRKTTLSRPVNVSVRLMTGFDL 319
QY 301 KKTLSYIGVSKIFEEHGLTKLAPHRSLKVGAEVHAELKMDERGTGAAGTGAQTLPM 360

DB 320 KKTLSYIGVSKIFEEHGDLTIKIAPHRSKVGAEVHKAELKMDERGETGAAGTLPME 379
QY 361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 395
DB 380 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 2
Q7TMFS_MOUSE PRELIMINARY; PRT; 413 AA.
AC Q7TMFS_MOUSE
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Visceral adipose-specific SERPIN.
GN Name=Serpin12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Swiss Webster;
RA Hida K., Wada J., Zhang H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; AY326419; AAP88383.1; -; mRNA.
DR HSSP; P01008; 1ATH.
DR MGI; MGI:1915304; Serpin12.
DR GO; GO:0005615; Extracellular space; TAS.
DR InterPro; IPR000295; Proc_inh_Leerp2.
DR InterPro; IPR000215; Proc_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR PRINTS; PR00780; LEUSERPINII.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
SQ Serpin.
KW SEQUENCE 413 AA; 47674 MW; EE2B3B08C2DD418F CRC64;

Query Match 4.8%; Score 19; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 325 HRSKVGAEVHKAELKMD 343
DB 344 HRSKVGAEVHKAELKMD 362

RESULT 3
Q9CQ32_MOUSE PRELIMINARY; PRT; 413 AA.
AC Q9CQ32_MOUSE
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632419J12 product:hypothetical Serpins containing protein, full insert sequence (Mus musculus 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3300001F13 product:hypothetical Serpins containing protein, full insert sequence).
GN Name=Serpin12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX MEDLINE=99279253; PubMed=10349656; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K., Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J., Schriml L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Bash G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Guernicich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S., Hayashizaki Y.;
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nagai K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake U.A., Brad D., Brusic V., Chotila C., Corbali L.B., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Guernicich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L., Kongaya A., Kurochkin I.V., Lee Y., Lehnard B., Lyons P.A., Maglott D.R., Malat L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numa K., Okido T., Pavan W.D., Pereira G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunaga H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6].
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA Adachi J., Mizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukumoto S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hirakawa T., Horii F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito R., Saito H., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tojima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; AK014589; BAB29447.1; -; mRNA.
DR EMBL; AK014346; BAB29287.1; -; mRNA.
DR HSSP; P01008; IATH.
DR Ensemble; ENSMUSG0000041567; Mus musculus.
DR MGI; MGI:1915304; Serpin12.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000295; Prot_inh_Leerp2.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR PRINTS; PR00780; LEUSERPINII.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR Hypoetical; protein; Serpin.
KW SEQUENCE 413 AA; 47634 MW; DOA8B1BE24FD60A CRC64;
SO
Query Match 4.8%; Score 19; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 325 HRSKVGSAVHAKELKXMD 343
Db 344 HRSKVGSAVHAKELKXMD 362

RESULT 4
06PEM3_MOUSE PRELIMINARY; PRT; 413 AA.
AC 06PEM3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Visceral adipose-specific SERPIN.
GN Name=Serpin12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Jaw and Limb;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
RA Klausner S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisla K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.B., Jones S.J.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2].
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Jaw and Limb;
RG NIH MGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; BC062143; AAH62143.1; -; mRNA.
DR HSSP; P01008; IATH.
DR Ensemble; ENSMUSG0000041567; Mus musculus.
DR MGI; MGI:1915304; Serpin12.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000295; Prot_inh_Leerp2.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR PRINTS; PR00780; LEUSERPINII.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SO SEQUENCE 413 AA; 47630 MW; CE1940BA2EB35811 CRC64;
Oy 325 HRSKVGSAVHAKELKXMD 343
Db 344 HRSKVGSAVHAKELKXMD 362

RESULT 5
08R4Z1_RAT PRELIMINARY; PRT; 411 AA.
AC 08R4Z1;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Visceral adipose tissue specific SERPIN.
GN Name=Serpin12; Synonyms=Vaspin;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OLETF; TISSUE=Visceral adipose;
RA Hida K., Wada J., Zhang H., Shikata K., Makino H.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; AF245398; AAU9574.1; -; mRNA.
DR HSSP; P01008; IATH.
DR Ensemble; ENSMUSG00000009710; Rattus norvegicus.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000295; Prot_inh_Leerp2.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR PRINTS; PR00780; LEUSERPINII.
DR SMART; SM00093; SERPIN; 1.

KW Serpin. 411 AA; 47527 MW; 29FA271FF8CC8A2D CRC64;
SQ SEQUENCE

Query Match 4.1%; Score 16; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 NIFLSPPLSISTAFSML 67
|||
71 NIFLSPPLSISTAFSML 86

Search completed: March 31, 2006, 10:07:43
Job time : 149.895 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 10:08:07 ; Search time 32.225 Seconds
(without alignments)
1013.403 Million cell updates/sec

Title: US-10-664-356-1562_COPY_20_414

Perfect score: 395

Sequence: 1 LKSPSPRYKALSEVQGM.....YSEKIPSVLFLGKIYVPIGK 395

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :

Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCJUS.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	395	100.0	414	2	US-09-755-665-14
2	395	100.0	414	2	US-09-755-665-55
3	395	100.0	414	2	US-09-755-665-56
4	395	100.0	415	2	US-09-461-325-134
5	395	100.0	415	2	US-10-012-542-134
6	395	100.0	415	2	US-10-115-123-134
7	310	78.5	361	2	US-09-755-665-57

ALIGNMENTS

RESULT 1
US-09-755-665-14
Sequence 14, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhir Das K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce B.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14

PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 14
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-14

Query Match 100.0%; Score 395; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	1LKSPSPRYKALSEVQGMQRMAAKELARQNDLGFKLKLAFLNPRGNIFLSPISI	60
DB	20	1LKSPSPRYKALSEVQGMQRMAAKELARQNDLGFKLKLAFLNPRGNIFLSPISI	79
QY	61	STAFSMLCLGADSTLDEIKGFNPRKPEKOLHGFYIITHELTKQTQDCLKSTIGTLF	120
DB	80	STAFSMLCLGADSTLDEIKGFNPRKPEKOLHGFYIITHELTKQTQDCLKSTIGTLF	139
QY	121	IDRLQPKRKELEDAKQFSAETILLTNQNLMAQKQINDPISQKTHKINNLENDPG	180
DB	140	IDRLQPKRKELEDAKQFSAETILLTNQNLMAQKQINDPISQKTHKINNLENDPG	199
QY	181	TVMLLANYIFPRAWKHEFDNVTKEBDFLEKXSVKVPMMFRSGIYQVYDCLKSTI	240
DB	200	TVMLLANYIFPRAWKHEFDNVTKEBDFLEKXSVKVPMMFRSGIYQVYDCLKSTI	259
QY	241	LEIPYQKNITAFILIPDEGKLKLEKGLQVDTFSRWTLISRRVVDVSPRLHMTGTEDL	300
DB	260	LEIPYQKNITAFILIPDEGKLKLEKGLQVDTFSRWTLISRRVVDVSPRLHMTGTEDL	319
QY	301	KKTLSTYIGSVKIFREHGDLTIAFHRSLKXGAVAHKAELKXDERGTGAAGTGLPME	360
DB	320	KKTLSTYIGSVKIFREHGDLTIAFHRSLKXGAVAHKAELKXDERGTGAAGTGLPME	379
QY	361	TPLVVKIDKPLLLIYSEKIPSVLFLGKIYVPIGK	395
DB	380	TPLVVKIDKPLLLIYSEKIPSVLFLGKIYVPIGK	414

RESULT 2
US-09-755-665-55
Sequence 55, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhir Das K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce B.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 55
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-55

Query Match 100.0%; Score 395; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LKSPSPRYKALSEVQGMQRMAAKELARQNDLGFKLKLAFLNPRGNIFLSPISI 60

Db 20 LKPSFSPRYKALSEVQGWKQMAKELARQNMDDGFLLKCLAFYNGRNIFLSPLSI 79
Qy 61 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFYIHELTOYKTDLKLISGNTLF 120
Db 80 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFYIHELTOYKTDLKLISGNTLF 139
Qy 121 IDORLOPQKFLLEDANKFYSAETILTNFQNLMAQKQINDFISQKTHGKINNLINENIDPG 180
Db 140 IDORLOPQKFLLEDANKFYSAETILTNFQNLMAQKQINDFISQKTHGKINNLINENIDPG 199
Qy 181 TWMLLANYIFFPRAWKHEPDNVTKEEDFLEKSSVYKVPMMFRSGIYGVYDDKLSCTI 240
Db 200 TWMLLANYIFFPRAWKHEPDNVTKEEDFLEKSSVYKVPMMFRSGIYGVYDDKLSCTI 259
Qy 241 LEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLSSRRVYDVSVRLHMTGTFDL 300
Db 260 LEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLSSRRVYDVSVRLHMTGTFDL 319
Qy 301 KKLSTYIGVSKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKMDRGTEGAAGTAQTLPME 360
Db 320 KKLSTYIGVSKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKMDRGTEGAAGTAQTLPME 379
Qy 361 TPLVWKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 395
Db 380 TPLVWKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 3

US-09-755-665-56
Sequence 56, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tailion, Bruce E.
APPLICANT: Spaderma, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-56

Query Match 100.0%; Score 395; DB 2; Length 414;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPSFSPRYKALSEVQGWKQMAKELARQNMDDGFLLKCLAFYNGRNIFLSPLSI 60
Db 20 LKPSFSPRYKALSEVQGWKQMAKELARQNMDDGFLLKCLAFYNGRNIFLSPLSI 79
Qy 61 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFYIHELTOYKTDLKLISGNTLF 120
Db 80 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFYIHELTOYKTDLKLISGNTLF 139
Qy 121 IDORLOPQKFLLEDANKFYSAETILTNFQNLMAQKQINDFISQKTHGKINNLINENIDPG 180
Db 140 IDORLOPQKFLLEDANKFYSAETILTNFQNLMAQKQINDFISQKTHGKINNLINENIDPG 199
Qy 181 TWMLLANYIFFPRAWKHEPDNVTKEEDFLEKSSVYKVPMMFRSGIYGVYDDKLSCTI 240
Db 200 TWMLLANYIFFPRAWKHEPDNVTKEEDFLEKSSVYKVPMMFRSGIYGVYDDKLSCTI 259

Qy 241 LEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLSSRRVYDVSVRLHMTGTFDL 300
Db 260 LEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLSSRRVYDVSVRLHMTGTFDL 319
Qy 301 KKLSTYIGVSKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKMDRGTEGAAGTAQTLPME 360
Db 320 KKLSTYIGVSKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKMDRGTEGAAGTAQTLPME 379
Qy 361 TPLVWKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 395
Db 380 TPLVWKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 4

US-09-461-325-134
Sequence 134, Application US/09461325A
Patent No. 6475753
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029P1
CURRENT APPLICATION NUMBER: US/09/461,325A
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: PCT/US99/13418
EARLIER FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 60/089,507
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,508
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,509
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,510
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: 60/090,113
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 134
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (415)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-461-325-134

Query Match 100.0%; Score 395; DB 2; Length 415;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPSFSPRYKALSEVQGWKQMAKELARQNMDDGFLLKCLAFYNGRNIFLSPLSI 60
Db 20 LKPSFSPRYKALSEVQGWKQMAKELARQNMDDGFLLKCLAFYNGRNIFLSPLSI 79
Qy 61 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFYIHELTOYKTDLKLISGNTLF 120
Db 80 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFYIHELTOYKTDLKLISGNTLF 139
Qy 121 IDORLOPQKFLLEDANKFYSAETILTNFQNLMAQKQINDFISQKTHGKINNLINENIDPG 180
Db 140 IDORLOPQKFLLEDANKFYSAETILTNFQNLMAQKQINDFISQKTHGKINNLINENIDPG 199
Qy 181 TWMLLANYIFFPRAWKHEPDNVTKEEDFLEKSSVYKVPMMFRSGIYGVYDDKLSCTI 240
Db 200 TWMLLANYIFFPRAWKHEPDNVTKEEDFLEKSSVYKVPMMFRSGIYGVYDDKLSCTI 259
Qy 241 LEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLSSRRVYDVSVRLHMTGTFDL 300
Db 260 LEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLSSRRVYDVSVRLHMTGTFDL 319

QY 301 KKTLSYIGVSKIPFEEHGDLTAKIAPHRSILKVGAVHKAELKMDERGTGGAAGTGLPME 360
DB 320 KKTLSYIGVSKIPFEEHGDLTAKIAPHRSILKVGAVHKAELKMDERGTGGAAGTGLPME 379
QY 361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 395
DB 380 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 5

US-10-012-542-134
; Sequence 134, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-012-542-134

Query Match 100.0%; Score 395; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKSPSPRYKALSEVQGWKQMAAKELARQNDLGFKLLKGLAFNPGRNIFLSPLSI 60
DB 20 LKSPSPRYKALSEVQGWKQMAAKELARQNDLGFKLLKGLAFNPGRNIFLSPLSI 79
QY 61 STAFSMCLGAOSTLDEIKQGFNFRMPKEDLHEGFHYIHLTQKTODLKISGNTLF 120
DB 80 STAFSMCLGAOSTLDEIKQGFNFRMPKEDLHEGFHYIHLTQKTODLKISGNTLF 139
QY 121 IDRLQPKRFLBDANKFYSAETILTNFQNLMAQKQINDFISQTHGKINNLIENIDPG 180
DB 140 IDRLQPKRFLBDANKFYSAETILTNFQNLMAQKQINDFISQTHGKINNLIENIDPG 199
QY 181 TWMLLANYIFFRARWGHFDPNVTKEEDFLEKNSSVKVPMMFRSGIYQGYDDKLSCTI 240
DB 200 TWMLLANYIFFRARWGHFDPNVTKEEDFLEKNSSVKVPMMFRSGIYQGYDDKLSCTI 259
QY 241 LEIPYQKNITAIIFLPDEGDKLHLEKGLQVDTFSRWKTLISRRVVDVSVRLHMTGTFDL 300
DB 260 LEIPYQKNITAIIFLPDEGDKLHLEKGLQVDTFSRWKTLISRRVVDVSVRLHMTGTFDL 319
QY 301 KKTLSYIGVSKIPFEEHGDLTAKIAPHRSILKVGAVHKAELKMDERGTGGAAGTGLPME 360
DB 320 KKTLSYIGVSKIPFEEHGDLTAKIAPHRSILKVGAVHKAELKMDERGTGGAAGTGLPME 379

QY 361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 395
DB 380 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 6

US-10-115-123-134
; Sequence 134, Application US/10115123
; Patent No. 674216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30APID2
; CURRENT APPLICATION NUMBER: US/10/115,123
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-115-123-134

Query Match 100.0%; Score 395; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKSPSPRYKALSEVQGWKQMAAKELARQNDLGFKLLKGLAFNPGRNIFLSPLSI 60
DB 20 LKSPSPRYKALSEVQGWKQMAAKELARQNDLGFKLLKGLAFNPGRNIFLSPLSI 79
QY 61 STAFSMCLGAOSTLDEIKQGFNFRMPKEDLHEGFHYIHLTQKTODLKISGNTLF 120
DB 80 STAFSMCLGAOSTLDEIKQGFNFRMPKEDLHEGFHYIHLTQKTODLKISGNTLF 139
QY 121 IDRLQPKRFLBDANKFYSAETILTNFQNLMAQKQINDFISQTHGKINNLIENIDPG 180
DB 140 IDRLQPKRFLBDANKFYSAETILTNFQNLMAQKQINDFISQTHGKINNLIENIDPG 199
QY 181 TWMLLANYIFFRARWGHFDPNVTKEEDFLEKNSSVKVPMMFRSGIYQGYDDKLSCTI 240
DB 200 TWMLLANYIFFRARWGHFDPNVTKEEDFLEKNSSVKVPMMFRSGIYQGYDDKLSCTI 259
QY 241 LEIPYQKNITAIIFLPDEGDKLHLEKGLQVDTFSRWKTLISRRVVDVSVRLHMTGTFDL 300
DB 260 LEIPYQKNITAIIFLPDEGDKLHLEKGLQVDTFSRWKTLISRRVVDVSVRLHMTGTFDL 319
QY 301 KKTLSYIGVSKIPFEEHGDLTAKIAPHRSILKVGAVHKAELKMDERGTGGAAGTGLPME 360
DB 320 KKTLSYIGVSKIPFEEHGDLTAKIAPHRSILKVGAVHKAELKMDERGTGGAAGTGLPME 379
QY 361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 395
DB 380 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 7

```
US-09-755-665-57
; Sequence 57: Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(361)
; OTHER INFORMATION: wherein Xaa is any amino acid as defined in the
; OTHER INFORMATION: specification
US-09-755-665-57
```

Query Match 78.5%; Score 310; DB 2; Length 361;

Best Local Similarity 100.0%; Pred. No. 8.1e-294;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 35 DLGFKLLKLAFLPFGNITLSPISSTAFSMLCLGAQDSTLDEIKGFNFRKMPKDLH 94
DB 1 DLGFKLLKLAFLPFGNITLSPISSTAFSMLCLGAQDSTLDEIKGFNFRKMPKDLH 60
QY 95 EGFHYIHELTKTODLKSIGNTLFLDRLQPKRFLBDKKNFYSATLLTNFQNLMA 154
DB 61 EGFHYIHELTKTODLKSIGNTLFLDRLQPKRFLBDKKNFYSATLLTNFQNLMA 120
QY 155 OKQINDFISQKTGKINNLINLIENTIDPGTVMLANIYIFPRARKHEFDPNVTKEEDFPLEKN 214
DB 121 OKQINDFISQKTGKINNLINLIENTIDPGTVMLANIYIFPRARKHEFDPNVTKEEDFPLEKN 180
QY 215 SSVKVPMMPFRSGIYQVGYDDKSLTILEIPYQKNITAIPLPDGKLLKLEKGLQVDTFS 274
DB 181 SSVKVPMMPFRSGIYQVGYDDKSLTILEIPYQKNITAIPLPDGKLLKLEKGLQVDTFS 240
QY 275 RKMTLLSRVVDVSVPLHMTGTFDLKKTLSYIGVSKIPREHGLTKIAPRSLKVGNAV 334
DB 241 RKMTLLSRVVDVSVPLHMTGTFDLKKTLSYIGVSKIPREHGLTKIAPRSLKVGNAV 300
QY 335 HKAEIIMDER 344
DB 301 HKAEIIMDER 310
```

Search completed: March 31, 2006, 10:09:52
Job time : 33.225 secs